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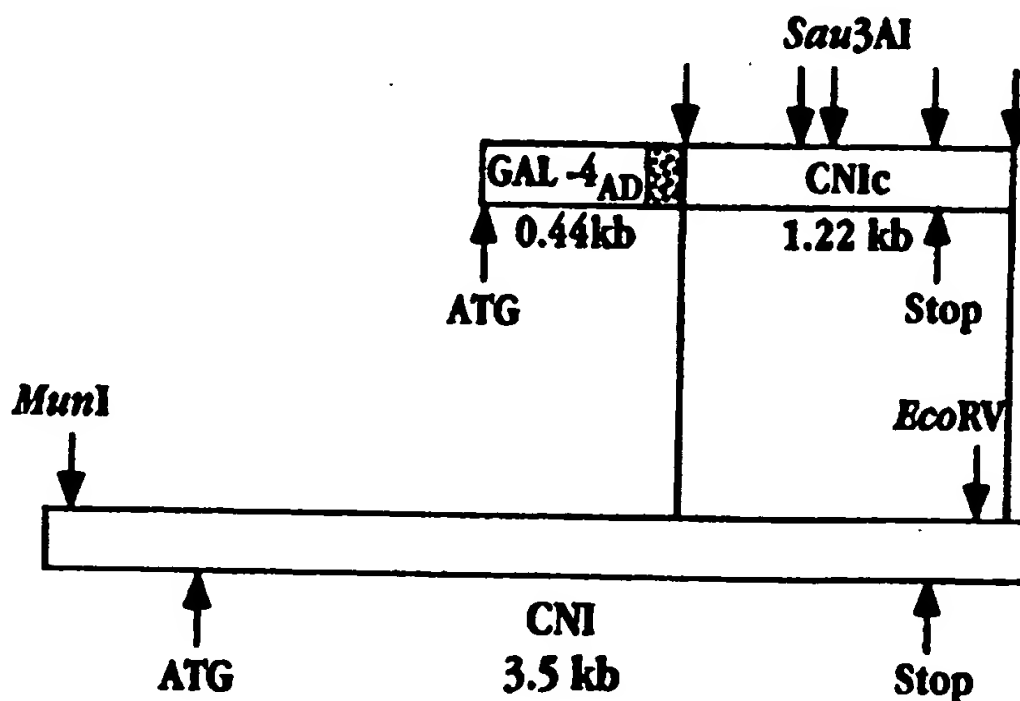
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(54) Title: CALCINEURIN INTERACTING PROTEIN COMPOSITIONS AND METHODS

(57) Abstract

An identification and characterization of a calcineurin interacting (CNI) protein effective to enhance immunosuppressive effects of calcineurin-targeted immunosuppressants by potentiating an interaction of an immunophilin with calcineurin is described herein. One embodiment of the invention is the CNI polypeptide encoded by the *CNI* gene of *Saccharomyces cerevisiae*. Polynucleotides encoding a CNI protein are also described. Also described are yeast cells carrying mutations in the *CNI* gene. Further, a method of identifying a small molecule immunosuppressant compound is described. The methods include the use of a cell-based two hybrid protein-protein interaction assay, wherein one of two fusion hybrid proteins in a cell contains a subunit of calcineurin, and the other of two fusion hybrid proteins contains an immunophilin.



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CALCINEURIN INTERACTING PROTEIN
COMPOSITIONS AND METHODS

Field of the Invention

- 5 The present invention relates to compounds affecting the function of calcineurin, particularly interactions of calcineurin with immunosuppressant drugs.

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30 Background of the Invention

The immune system functions as the body's major defense against diseases caused by invading organisms. This complex system fights disease by killing invaders such as bacteria, viruses, parasites or cancerous cells while leaving the body's normal tissues unharmed. The immune system's ability to distinguish the body's normal tissues, or self, from foreign or

cancerous tissue, or non-self, is an essential feature of normal immune system function. A second essential feature is memory, the ability to remember a particular foreign invader and to mount an enhanced defensive response when the previously encountered invader returns. The loss of recognition of a particular tissue as self and the subsequent immune response directed against that tissue produce serious illness.

An autoimmune disease results from the immune system attacking the body's own organs or tissues, producing a clinical condition associated with the destruction of that tissue. An autoimmune attack directed against the joint lining tissue results in rheumatoid arthritis; an attack against the conducting fibers of the nervous system results in multiple sclerosis. The autoimmune diseases most likely share a common pathogenesis and the need for safe and effective therapy. One type of therapy that has been employed in combating autoimmune disease is treatment with immunosuppressant drugs, such as cyclosporin A, FK506 and rapamycin. While the treatments are often effective, the drugs typically have undesirable side effects, including neurotoxicity, nephrotoxicity, hypertension, and metabolic disorder. Many of these side effects are due to the drugs' action on cells other than those of the immune system.

In addition to their use in treating autoimmune conditions, immunosuppressive agents have also been used in treating or preventing transplantation rejection. Organ transplantation involving human organ donors and human recipients (allogeneic grafts), and non-human primate donors and human recipients (xenogeneic grafts), has received considerable medical and scientific attention (*e.g.*, Roberts, 1989; Platt, 1990). To a great extent, this effort has been aimed at eliminating, or at least reducing, the problem of rejection of the transplanted organ. In the absence of adequate immunosuppressive therapy, the transplanted organ is destroyed by the host immune system.

Presently, the most commonly used agents for preventing transplant rejection include corticosteroids, cytotoxic drugs that specifically inhibit T cell activation such as azathioprine, immunosuppressive drugs such as cyclosporin A, and specific antibodies directed against T lymphocytes or surface receptors that mediate their activation (Briggs, 1991; Kennedy, 1983; Storb, 1985; Storb, 1986). All of these drug therapies are limited in effectiveness, in part because the doses needed for effective treatment of transplant rejection may increase the patient's susceptibility to infection by a variety of opportunistic invaders, and in part because of direct toxicity and other side effects.

Cyclosporin A, currently the most effective and most commonly used agent, is significantly toxic to the kidney. This nephrotoxicity limits the quantity of drug that can be

safely given. The physician is frequently forced to administer sub-optimal doses of the drug because of this toxicity. A preparation capable of potentiating the action of immunosuppressive agents such as cyclosporin A on the immune system, thus allowing the administration of lower doses of drug, would be of considerable value in reducing the morbidity and mortality associated with transplantation.

Summary of the Invention

In one embodiment, the present invention includes polypeptide compositions effective to enhance immunosuppressive effects of calcineurin-targeted immunosuppressants by potentiating an interaction of an immunophilin with calcineurin. The present invention includes the isolation and characterization of a calcineurin interacting protein, CNI, having these properties. Also disclosed herein are methods for the isolation and characterization of further CNI-related sequences and sequences of CNI-variants. The amino acid sequences presented as SEQ ID NO:2 and SEQ ID NO:5 are exemplary of the polypeptides of the present invention.

The present invention also includes a CNI polypeptide fragment that interacts specifically with the "A" subunits of calcineurin (CNA1 and CNA2), but not with calcineurin "B" subunit (CNB1). In one embodiment, this fragment has an amino acid sequence of between 15 and 915 amino acids in length, for example, the c-terminal 306 amino acids of the CNI protein (CN1c).

Included aspects of the invention are an CNI polypeptide; a recombinant CNI polypeptide; and a fusion polypeptide comprised of an CNI polypeptide. Exemplary fusion proteins include fusions to β -galactosidase.

The invention further includes isolated nucleic acid sequences encoding the above described polypeptides and polypeptide fragments. Exemplary nucleic acid sequences include the sequences presented as SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4 and SEQ ID NO:6. The present invention includes CNI-encoding genomic polynucleotides, cDNAs thereto and complements thereof. With respect to polynucleotides, some aspects of the invention include: a purified CNI-encoding genomic polynucleotide; CNI polypeptide-encoding RNA and DNA polynucleotides; recombinant CNI polypeptide-encoding polynucleotides; a recombinant vector including any of the above recombinant polynucleotides, and a host cell transformed with any of these vectors. Another aspect of the invention is a polynucleotide probe for CNI polypeptide-encoding sequences.

Portions of a CNI-polypeptide coding sequences are effective as probes to isolate variants coding sequences which occur naturally, or to determine the presence of such coding

sequences in nucleic acid samples. Such probes include hybridization screening probes and polymerase chain reaction amplification primers specific for CNI-polypeptide coding sequences. Homologues of CNI may be isolated from a number of sources, such as other types of yeast cells (*e.g.*, *Schizosaccharomyces*) or mammalian cells (*e.g.*, human).

5 Other aspects of the invention include: a recombinant expression system which incorporates an open reading frame (ORF) derived from CNI polypeptide-encoding sequences, wherein the ORF is linked operably to a control sequence which is compatible with a desired host, a cell transformed with the recombinant expression system, and a polypeptide produced by the transformed cell. Typically the expression system includes a vector having (a) a nucleic
10 acid containing an open reading frame that encodes a CNI-polypeptide; and (b) regulatory sequences effective to express said open reading frame in a host cell. The regulatory sequence may include sequences useful for targeting or secretion of the CNI-polypeptide: such as a secretory signal recognized in yeast or bacterial expression systems.

The invention includes a method of recombinantly producing CNI-polypeptides. In the
15 method, a recombinant expression system containing an open reading frame (ORF) having a polynucleotide sequence which encodes a CNI-polypeptide, where the vector is designed to express the ORF in the host, is introduced into suitable host cells. The host is then cultured under conditions resulting in the expression of the ORF sequence. The CNI-polypeptide sequences discussed above are examples of suitable CNI-polypeptides. Numerous vectors and
20 their corresponding hosts are useful in the practice of this method of the invention, including, but not limited, to the vectors described herein for expression in yeast cells, and lambda gt11 phage vector and *E. coli* cells. Other host cells include insect and mammalian cell expression systems.

The invention also includes purified antibodies that are immunoreactive with a CNI-
25 polypeptide. The antibodies may be polyclonal or monoclonal. Antibodies that are specifically immunoreactive with CNI-polypeptides may be useful for the isolation of CNI-polypeptide homologues from other cell type sources (*e.g.*, mammalian).

The present invention also includes, a method of identifying a small molecule immunosuppressant compound. In the method, a cell-based two hybrid protein-protein
30 interaction assay is constructed where one of two fusion hybrid proteins in the cell contains a subunit of calcineurin, and the other of two fusion hybrid proteins contains an immunophilin. The cell is then contacted with the small molecule being tested. A small molecule is identified as an immunosuppressant if the molecule potentiates an interaction between the two hybrid proteins. In one embodiment, the method is carried out using yeast cells, where one of the two

fusion hybrid proteins contains a GAL4 activation domain and the other of two fusion hybrid proteins contains a GAL4 binding domain. The method can be carried out where subunits of calcineurin are from any cell source, in particular, yeast or mammalian cells (including human cells). The subunit may, for example, be yeast calcineurin subunit CNA1 or CNA2, or human
5 calcineurin subunit "A". The immunophilin can, for example, be cyclophilins or FK506-binding proteins (*e.g.*, FKBP12) typically from a homologous cell source.

Also included in the present invention is another method of identifying a small molecule immunosuppressant compound. In the method, a cell-based two hybrid protein-protein interaction assay is constructed, wherein one of two fusion hybrid proteins in a cell contains
10 an "A" subunit of calcineurin, and the other of two fusion hybrid proteins contains a CNI polypeptide. The cell preferably, but not necessarily, also contains a vector construct causing overexpression, or increased expression, of a "B" subunit of calcineurin. The cell is then contacted with the small molecule being tested. A small molecule is identified as an immunosuppressant if the molecule potentiates an interaction between the two hybrid proteins.

15 This method is used to identify compounds (like FK506) that potentiate the interaction between CNI and CNA1. In one embodiment, the method is carried out using yeast cells, where one of the two fusion hybrid proteins contains a GAL4 activation domain and the other of two fusion hybrid proteins contains a GAL4 binding domain. The method can be carried out where subunits of calcineurin are from any cell source, in particular, yeast or mammalian cells
20 (including human cells). The subunits may, for example, be calcineurin subunit A1 or A2. The CNI polypeptide may also be from any source (*e.g.*, yeast or human), and may be only a fragment of a complete CNI polypeptide (such as a c-terminal fragment). An exemplary c-terminal fragment of CNI is CN1c.

Further, included in the present invention, is a yeast cell carrying a mutation in the
25 naturally-occurring copy of *CNI*, where the mutation prevents expression of a functional CNI protein from the genomic copy. Embodiments of this aspect of the present invention include deletion mutations within the coding region of the *CNI* gene, deletion of regulation regions of the *CNI* gene, and non-sense or mis-sense mutations in the *CNI* gene. Yeast cells having such mutations are useful, for example, in a method of identifying proteins of similar function to
30 CNI. In one embodiment, a hybrid interaction screen is set up in a cell with a CNI deletion and a GAL4 protein binding domain-CNA fusion and a GAL4 activation domain-immunophilin fusion. Expression libraries are then screened to identify clones encoding proteins that potentiate an interaction of an immunophilin with calcineurin. This screen will identify CNI-coding sequences as well as other proteins with a similar function.

In a related embodiment, a yeast cell with a CNI deletion is used to identify CNI homologues (e.g., from other organisms, such as human) using a complementation assay or screen. Expression libraries (e.g., human lymphocyte expression libraries) are transformed into cells with a CNI deletion, and transformants are selected on their ability to complement the function of yeast CNI. An exemplary assay for selecting such transformants is exposure to hygromycin B. Cells which become more sensitive to hygromycin B following transformation are further analyzed to determine if the plasmid with which they were transformed contains an insert homologous to yeast CNI, or encoding a polypeptide with similar function to CNI.

The invention also includes a yeast cell carrying a mutation in the naturally-occurring genomic copy of a gene encoding calcineurin-interacting polypeptide, where the mutation prevents expression of a functional calcineurin-interacting polypeptide from the genomic copy. The mutation may be a null mutation, such as described in Example 8 below, or a different type of mutation, e.g., a nonsense or missense mutation. Nonsense and missense mutations may be generated using standard methods.

These and other objects and features of the invention will be more fully appreciated when the following detailed description of the invention is read in conjunction with the accompanying drawings.

Brief Description of the Figures

Figures 1A and 1B present schematic diagrams of sequences encoding the c-terminal portion of CNI (CN1c) fused to GAL-4 activation domain (GAL-4AD) (Fig. 1A), and sequences encoding CNI (Fig. 1B).

Figure 2A presents data from a β -galactosidase (β -gal) assay to detect the interaction of CN1c with the A1 subunit of calcineurin (CNA1), A2 subunit of calcineurin (CNA2), GAL-4 binding domain (G4BD) and lamin C. A labeled schematic diagram corresponding to the data shown in Fig. 2A is presented in Fig. 2B to facilitate reference to individual groups of colonies.

Figure 3A presents data from a β -gal assay to detect the interaction of CN1c with CNA1 Δ C, CNA2 Δ C and CNB1. A labeled schematic diagram corresponding to the data shown in Fig. 3A is presented in Fig. 3B.

Figures 4A and 4C present data from β -gal assays to evaluate the effects of FK506 and the deletion of CNB1 on the interactions of CN1c with CNA and CNA Δ C. Labeled schematic diagrams corresponding to the data shown in Figs. 4A and 4C are presented in Figs. 4B and 4D, respectively.

Figures 5A and 5C present data from β -gal assays to evaluate the effects of FK506 and the overexpression of CNB1 on the interactions of CN1c with CNA and CNA Δ C. Labeled schematic diagrams corresponding to the data shown in Figs. 5A and 5C are presented in Figs. 5B and 5D, respectively.

5 Figures 6A, 6C and 6E present data from β -gal assays to evaluate the effects of FK506, cyclosporin A (CsA), and the deletion of CNB1 on the interaction of CN1c with CNA and CNA Δ C. Labeled schematic diagrams corresponding to the data shown in Figs. 6A, 6C and 6E are presented in Figs. 6B, 6D and 6F, respectively.

10 Figures 7A, 7C, 7E and 7G present data from β -gal assays to evaluate the effects of FK506, cyclosporin A (CsA), rapamycin and the overexpression of CNB1 on the interaction of CN1c with CNA and CNA Δ C. Labeled schematic diagrams corresponding to the data shown in Figs. 7A, 7C, 7E and 7G are presented in Figs. 7B, 7D, 7F and 7H, respectively.

15 Figure 8A presents data from a β -gal assay to evaluate the effects of overexpression of full-length CNI on FK506-dependent interaction of FKBP with CNA. A labeled schematic diagram corresponding to the data shown in Fig. 8A is presented in Fig. 8B.

Figures 9A and 9C present data from β -gal assays to evaluate the effects of overexpression of full-length CNI on FK506-dependent interaction of FKBP with CNB1. Labeled schematic diagrams corresponding to the data shown in Figs. 9A and 9C are presented in Figs. 9B and 9D, respectively.

20 Figure 10 presents an image of a protein blot of CN1c and CNA co-immunoprecipitate probed with anti-CNA2 antibody.

Figure 11 presents an image of a yeast RNA blot hybridized with a CN1c probe.

Figure 12 presents the DNA sequence of a 3.5 kb fragment of yeast chromosome 11 containing the coding sequence for a yeast CNI protein.

25 Figure 13 presents the amino acid sequence of a yeast CNI protein.

Brief Description of the Sequences

SEQ ID NO:1 presents the nucleotide sequence of a *Sau3AI* fragment containing the coding sequence for CN1c.

30 SEQ ID NO:2 presents the amino acid sequence of CN1c encoded by SEQ ID NO:1.

SEQ ID NO:3 presents the coding sequence presented in SEQ ID NO:1.

SEQ ID NO:4 presents the nucleotide sequence of a gene encoding a complete CNI protein.

SEQ ID NO:5 presents the amino acid sequence encoded by SEQ ID NO:4.

SEQ ID NO:6 presents the coding sequence presented in SEQ ID NO:4.

SEQ ID NO:7 presents the nucleotide sequence of PCR primer CNI-PCR-A.

SEQ ID NO:8 presents the nucleotide sequence of PCR primer CNI-PCR-B.

5 SEQ ID NO:9 presents the nucleotide sequence of a gene encoding the yeast CNA1 subunit of calcineurin.

SEQ ID NO:10 presents the amino acid sequence encoded by SEQ ID NO:9.

SEQ ID NO:11 presents the nucleotide sequence of a gene encoding the yeast CNA2 subunit of calcineurin.

SEQ ID NO:12 presents the amino acid sequence encoded by SEQ ID NO:11.

10 SEQ ID NO:13 presents the nucleotide sequence of a gene encoding the yeast CNB1 subunit of calcineurin.

SEQ ID NO:14 presents an amino acid sequence encoded by SEQ ID NO:13.

SEQ ID NO:15 presents an amino acid sequence encoded by SEQ ID NO:13.

SEQ ID NO:16 presents the coding sequence presented in SEQ ID NO:13.

15 SEQ ID NO:17 presents the amino acid sequence encoded by SEQ ID NO:16.

SEQ ID NO:18 presents a nucleotide sequence encoding CNA1Δc.

SEQ ID NO:19 presents the amino acid sequence encoded by SEQ ID NO:18.

SEQ ID NO:20 presents a nucleotide sequence encoding CNA2Δc.

SEQ ID NO:21 presents the amino acid sequence encoded by SEQ ID NO:20.

20 SEQ ID NO:22 presents the nucleotide sequence of PCR primer G4-PCR-A.

SEQ ID NO:23 presents the nucleotide sequence of PCR primer G4-PCR-B.

Detailed Description of the Invention

I. DEFINITIONS

25 A "calcineurin-targeted immunosuppressant" is a compound that possesses *in vivo* immunosuppressive activity, and that interacts with an immunophilin to form a complex which is capable of inhibiting calcineurin.

"Interacting proteins" are proteins capable of specifically binding to one another, or associating with one another, in a cell or *in vitro*.

30 A calcineurin interacting (CNI) protein or polypeptide is a protein or polypeptide that is effective to enhance immunosuppressive effects of a calcineurin-targeted immunosuppressant by potentiating an interaction of an immunophilin with calcineurin. Preferably, a CNI protein or polypeptide is a protein or polypeptide having an amino acid sequence that is homologous to the sequence presented herein as SEQ ID NO:5.

"Substantially isolated" is used in several contexts and typically refers to the at least partial purification of a CNI protein or polypeptide fragment away from unrelated or contaminating components (*e.g.*, cytoplasmic contaminants and heterologous proteins). Methods and procedures for the isolation or purification of compounds or components of interest are described below (*e.g.*, affinity purification of fusion proteins and recombinant production of CNI polypeptides).

In the context of the present invention, the phrase "nucleic acid sequences," when referring to sequences which encode a protein, polypeptide, or peptide, is meant to include degenerative nucleic acid sequences which encode homologous protein, polypeptide or peptide sequences as well as the disclosed sequence.

Two nucleic acid fragments are considered to have "homologous" sequences if they are capable of hybridizing to one another (i) under typical hybridization and wash conditions, as described, for example, in Sambrook, *et al.*, pages 320-328, and 382-389, or (ii) using reduced stringency wash conditions that allow at most about 25-30% basepair mismatches, for example: 2 × SSC, 0.1% SDS, room temperature twice, 30 minutes each; then 2 × SSC, 0.1% SDS, 37°C once, 30 minutes; then 2 × SSC, room temperature twice, 10 minutes each. Preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches. These degrees of homology can be selected by using wash conditions of appropriate stringency for identification of clones from gene libraries (or other sources of genetic material), as is well known in the art.

Two amino acid sequences or two nucleotide sequences (in an alternative definition for homology between two nucleotide sequences) are considered homologous (as this term is preferably used in this specification) if they have an alignment score of >5 (in standard deviation units) using the program ALIGN, typically default mutation gap matrix and gap penalty (Dayhoff). The two sequences (or parts thereof) are more preferably homologous if their amino acids are greater than or equal to 40% using the ALIGN program mentioned above.

II. OVERVIEW OF INVENTION

Experiments performed in support of the present invention demonstrate the identification and isolation of the nucleic acid sequence encoding a calcineurin interacting (CNI) protein. Further experiments performed in support of the present invention characterize the CNI protein, as well as a polypeptide containing only the c-terminal 306 amino acids of the CNI protein (CN1c). The experiments demonstrate that CN1c interacts specifically with the "A" subunits of calcineurin (CNA1 and CNA2), but not with calcineurin "B" subunit (CNB1).

The experiments also demonstrate that CN1c does not interact directly with FK506 binding protein (FKBP; Schreiber, *et al.*; with or without FK506), GAL4 binding domain (G4_{BD}) or lamin C. The experiments also demonstrate that CN1c interacts with C-terminally truncated forms of CNA (CNA Δ C), which have lost their autoinhibitory domains, though the interaction
5 is somewhat weaker than with full length CNA proteins.

Additional experiments show that the interaction between CN1c and CNA is enhanced when CNB1 is deleted, and diminished when CNB1 is overexpressed, that the interaction between CN1c and CNA or CNA Δ C is markedly enhanced by FK506 and by Cyclosporin A (CsA), but not rapamycin, and that overexpression of a full-length CNI protein enhances the
10 interaction between CNA and FKBP (detectable only in the presence of FK506).

Additional experiments conducted in support of the present invention demonstrate that overexpression of the full-length CNI has no detectable effect on the interaction between CNB1 and CNA, and that in the presence of FK506 or CsA, overexpression of CNB1 no longer inhibits the interaction of CN1c with CNA.

15 It was also found that CNI deletion mutants are viable, both in wild-type and CN-deletion backgrounds, and that CNI deletion mutants in a CN-deletion background are more resistant to hygromycin B than normal CN-deletion mutants.

Co-immunoprecipitation experiments demonstrate that CN1c and CNA co-immunoprecipitate in the presence of FK506, and protein blot experiments show that CNI is expressed at
20 low levels *in vivo*. RNA blot experiments show that CNI is encoded by a single message approximately 2.9 kb in length.

A comparison of the yeast CNI sequence with sequences present in nucleic acid and amino acid databases reveals no obvious homologous sequences have been identified in other
25 organisms.

III. CALCINEURIN

Experiments performed in support of the present invention were designed to identify polypeptides capable of interacting with calcineurin. Calcineurin (also called phosphoprotein phosphatase 2B or PP2B), has been characterized from many different tissues and organisms
30 (Klee, *et al.*). It is a heterodimer of two subunits, of which the "A" subunit is about 61 kD in weight, possesses catalytic activity and also contains the association site for calmodulin. The "B" subunit contains four Ca²⁺ binding sites and activates the A subunit. Calcineurin has little enzymatic activity, even in the presence of Ca²⁺ and only becomes fully active when associated with calmodulin (Cyert).

Two A subunits (CNA1 and CNA2; Cyert, *et al.*, 1991) and one B subunit (CNB1, Cyert, *et al.*, 1992) have been cloned in yeast. Either CNA1 or CNA2 may associate with CNB1 to form a functional calcineurin heterodimer. Multiple isotypes of the A subunit have been cloned from a variety of organisms and are highly conserved (Klee, *et al.*). In particular, calcineurin subunits have been cloned from human tissue (see reviews by, for example, Klee, *et al.*, and Guerini, *et al.*).

IV. IMMUNOSUPPRESSANT DRUGS

FK506, cyclosporin A (CsA) and rapamycin, derived from fungi, inhibit the activation of T-cells by antigens. The compounds have proven highly effective at suppressing mammalian immune systems *in vivo*. In particular, CsA therapy in clinical settings has dramatically increased the success rate of transplantation therapy.

It is now known that FK506 and CsA exert their immunosuppressive effects, in part, by inhibiting the transcriptional activation of the interleukin-2 (IL-2) gene, whereas rapamycin appears to function by inhibiting the response of T-cells to IL-2, presumably by inhibiting a transduction pathway mediated by the IL-2 receptor.

The molecular mechanism of FK506 and CsA immunosuppressive action involves a group of small, abundant intracellular proteins termed immunophilins, which bind with a high affinity to the immunosuppressants (Schreiber). At least two classes of immunophilins are known to exist. One class, termed cyclophilins, binds to CsA, while another class, the FK506-binding proteins (FKBPs) binds FK506 and rapamycin. Many immunophilin genes, from a variety of organisms, have been cloned, and appear to be highly conserved from simple eukaryotes to mammals.

It is believed that FK506 and CsA-induced immunosuppression is due to the binding of complexes, formed by binding of immunosuppressants FK506 and CsA bound to one of their respective immunophilins, to the catalytic subunit of calcineurin (Schreiber, *et al.*, Liu, *et al.*, Foor, *et al.*, Weiss, *et al.*). The binding of such a complex to an (A) subunit inhibits activation of calcineurin by increased intracellular calcium, which in turn prevents calcineurin from activating transcription factor NF-AT. Since IL-2 is one of the genes controlled by NF-AT in T-cells, inhibition of the transcription factor inhibits the production of IL-2, resulting in immunosuppression (Clipstone, *et al.*).

FK506 and CsA are widely used in organ transplantation to prevent host rejection. However, both drugs are known to have many undesired side-effects such as neurotoxicity, nephrotoxicity, hypertension, and metabolic disorder. Accordingly formulations effective to

increase a target cell's sensitivity to these drugs may be useful in alleviating some of the aforementioned side-effects. Specifically, CNI and its homologues or derivatives, administered at appropriate levels, may be able to increase the sensitivity of CN to FK506/CsA and reduce the necessary dosage thus reducing or eliminating the side-effects of these drugs.

5

V. TWO HYBRID PROTEIN INTERACTION ASSAYS

Two hybrid protein interaction assay methods (two hybrid protein-protein interaction screens) provide a simple and sensitive means to detect the interaction between two proteins in living cells. The assays are based on the finding that most eukaryotic transcription activators are modular (e.g., Brent, *et al.*), *i.e.*, that the activators typically contain activation domains that activate transcription, and DNA binding domains that localize the activator to the appropriate region of a DNA molecule.

The development of two hybrid protein interaction assays was made possible by the observation that the DNA binding domain does not need to be physically located on the same polypeptide as the activation domain (Ma, *et al.*, Triezenberg, *et al.*), raising the possibility that transcription of reporter genes could be used as an assay to detect protein interactions.

The utility of two hybrid systems for detecting interactions between two interacting proteins was fully realized by the observation that protein interactions could be detected if two potentially-interacting proteins were expressed as fusions, or chimeras (Fields, *et al.*). A first fusion protein contains one of a pair of interacting proteins fused to a DNA binding domain, and a second fusion protein contains the other of a pair of interacting proteins fused to a transcription activation domain. The two fusion proteins are independently expressed in the same cell, and interaction between the "interacting protein" portions of the fusions reconstitute the function of the transcription activation factor, which is detected by activation of transcription of a reporter gene.

At least two different cell-based two hybrid protein-protein interaction assay systems have been used to assess binding interactions and/or to identify interacting proteins. Both employ a pair of fusion hybrid proteins, where one of the pair contains a first of two "interacting" proteins fused to a transcription activation domain of a transcription activating factor, and the other of the pair contains a second of two "interacting" proteins fused to a DNA binding domain of a transcription activating factor.

The yeast GAL4 two hybrid system (Fields, *et al.*, Chien, *et al.*, Durfee, *et al.*, Bartel, *et al.*), utilized for experiments performed in support of the present invention, was developed

to detect protein-protein interaction based on the reconstitution of function of GAL4, a transcriptional activator from yeast, by activation of a *GAL1-lacZ* reporter gene.

Like several other transcription activating factors, GAL4 contains two distinct domains, a DNA binding domain and a transcription activation domain. Each domain can be independently expressed as a portion of a fusion protein composed of the domain, and a second, "bait" interacting protein. The two fusion proteins are then independently expressed together in a cell. When the two GAL4 domains are brought together by a binding interaction between the two "interacting" proteins, transcription of a reporter gene under the transcriptional control of GAL4 is initiated. The reporter gene typically has a promoter containing GAL4 protein binding sites (GAL upstream activating sequences, UAS₀). Exemplary reporter genes are the *GAL1-lacZ*, and *GAL1-HIS3* reporter genes used in experiments described herein.

A second two hybrid system, described in detail in Ausubel, *et al.*, utilizes a native *E. coli* LexA repressor protein, which binds tightly to appropriate operators. A plasmid is used to express one of a pair of interacting proteins (the "bait" protein) as a fusion to LexA. The plasmid expressing the LexA-fused bait protein is used to transform a reporter strain of yeast, such as EGY48, that contains pSH18-34.

In this strain, binding sites for LexA are located upstream of two reporter genes. In the first reporter system, the upstream activation sequences of the chromosomal LEU2 gene—required in the biosynthetic pathway for leucine (Leu)—are replaced in EGY48 with *lexA* operators, permitting selection for viability when cells are plated on medium lacking Leu. In the second reporter system, EGY48 harbors a plasmid, pSH18-34, that contains a *lexA* operator-*lacZ* fusion gene, permitting discrimination based on color when the yeast is grown on medium containing Xgal (Ausubel, *et al.*).

To screen a library with the LexA system, the library uses the inducible yeast GAL1 promoter to express proteins as fusions to an acidic domain ("acid blob") that functions as a portable transcriptional activation motif ("act"), and to other useful moieties. Expression of library-encoded proteins is induced by plating transformants on medium containing galactose (Gal), so yeast cells containing library proteins that do not interact specifically with the bait protein fail to grow in the absence of Leu. Yeast cells containing library proteins that interact with the bait protein form colonies within 2 to 5 days, and the colonies turn blue when the cells are streaked on medium containing Xgal. The plasmids are isolated and characterized by a series of tests to confirm specificity of the interaction with the initial bait protein. Those found to be specific are ready for further analysis (e.g., sequencing).

LexA and GAL4 each have different properties that should be considered when selecting a system. LexA is derived from a heterologous organism, has no known effect on the growth of yeast, possesses no residual transcriptional activity, can be used in GAL4⁺ yeast, and can be used with a Gal-inducible promoter. Because GAL4 is an important yeast transcriptional activator, experiments must be performed in *gal4* yeast strains to avoid background from endogenous GAL4 activating the reporter system.

Both two hybrid systems have been successfully used for isolating genes encoding proteins that bind a target protein and as simple protein binding assays (*e.g.*, Yang, *et al.*, Gyuris, *et al.*), and both can be applied to methods of the present invention.

Both gene isolation and protein binding assay applications of the GAL4 system are described in Examples below.

VI. SPECIFIC EMBODIMENTS

Example 1 demonstrates application of an exemplary two hybrid protein-protein interaction screen (Materials and Methods, section D) to the screening of three pGAD yeast fusion libraries, carrying fusions between the transcription activating domain of yeast protein GAL4 (G4AD) and yeast genomic DNA *Sau3A*I fragments, in all three reading frames. The libraries are screened to identify polypeptides, encoded by the *Sau3A*I fragments, capable of interacting with catalytic (A) subunits of calcineurin, expressed as fusions with the GAL4 protein binding domain (GBT-CNA fusions).

Three sets of yeast cells harboring pGBT-CNA1 *TRP1* (GBT-A1) hybrid plasmid and a GAL4-activated LacZ reporter gene are each transformed with one of the three reading-frame libraries. Construction of the plasmids used is described in Materials and Methods, sections B and C. Cells transformed with a plasmid encoding a protein fusion capable of interacting with the CNA subunit fusion are selected using a β -galactosidase (β -gal) assay on plates containing the chromogenic substrate X-gal (Materials and Methods, section E). Results of the β -gal assay are confirmed using a growth assay (Materials and Methods, section F). False positives are eliminated by colony purification (re-streaking for single colonies), PCR experiments using GAL4 primers, and testing against a number of test fusions by β -gal assays on transformed haploid or mated diploid reporter strains.

A yeast clone encoding a polypeptide capable of specifically interacting with CNA polypeptide fusions is identified and sequenced. The sequence of the *Sau3A*I fragment is presented as SEQ ID NO:1. The coding sequence forming the open reading frame is presented as SEQ ID NO:3. The polypeptide encoded by the open reading frame is presented as SEQ

ID NO:2. The open reading frame encodes 306 amino acids followed by a stop codon in frame with the coding sequence of GAL4, but does not contain an in-frame ATG start site upstream of the stop codon. This is consistent with the fragment encoding a c-terminal portion of a complete gene product. The clone is termed CNlc, with the lowercase "c" representing "c-terminal".

Figure 1A shows a schematic representation of the nucleic acid sequence encoding the GAL4AD-CNlc fusion protein. The stippled portion between GAL4AD and CNlc represents a linker discussed in the Materials and Methods section, as well as in Example 1. Also indicated in the Figure are the approximate locations of in-frame start (ATG) and stop codons, and *Sau3AI* restriction sites.

Example 1 further describes the identification of a λ clone encoding a full length sequence version of CNlc, termed CNI. The polypeptide encoded by the sequence is termed CNI protein. The clone is identified by hybridization screening of a panel of λ clones spanning the yeast genome using a 1.22 kb ^{32}P -labeled probe generated from CNlc.

Phage lysates of the λ clone are amplified, purified, restriction-mapped and used as a DNA source for subsequent cloning experiments. A 3.16 kb *MunI/EcoRV* fragment from the λ clone insert contains the coding sequence of CNI. The sequence of the 3.16 kb *MunI/EcoRV* fragment is encompassed by the 3.5 kb sequence presented as SEQ ID NO:4, and a schematic diagram of the sequence is shown in Figure 1B. This sequence contains the entire 2.75 kb coding sequence of CNI (SEQ ID NO:6; graphically indicated in Figure 1B by the locations of the "ATG" and "Stop" codons).

A search of known DNA and protein sequences turns up no obvious matches or homologies to genes in other organisms. Accordingly, CNI may represent a new type of calcineurin interacting protein.

The methods referred to above may also be applied to the screening of, for example, a human cDNA library using an appropriate two-hybrid protein interaction screen. The "bait" protein in the interaction screen (*e.g.*, the protein analogous to CNA1 in Example 1) may be of yeast origin (*e.g.*, CNA1), but is preferably of human origin (*e.g.*, a human calcineurin "A" subunit; Klee, *et al.*). The bait protein is expressed in the cell (*e.g.*, a yeast cell) used for the two hybrid interaction screen as a fusion to a domain of a transcription activating factor (*e.g.*, the DNA binding domain of GAL4). The library may be a human DNA library in a vector (*e.g.*, pGAD) effective to express library sequences as fusions to a complimentary domain of the transcription activating factor (*e.g.*, the activation domain of GAL4). Libraries of human sequences can be derived from a number of sources including genomic DNA, such as yeast

artificial chromosome (YAC) constructs carrying genomic human DNA, or cDNA generated from a variety of cell types (*e.g.*, activated T-cells).

Example 2 details a β -gal assay to determine the specificity of binding of CN1c to subunits of calcineurin. Exemplary results are shown in Figure 2A. The legend for Fig. 2A is shown in Figure 2B. Numbers in the legend refer to locations of yeast colonies expressing particular combinations of plasmid constructs (indicated in Example 2).

A comparison of the intensities of the blue β -gal reaction product indicates that CN1c interacts strongly with CNA1 (21, 22 and 23), and somewhat less strongly with CNA2 (24). Neither cells containing AS-lamin with GAD-CN1c (25), nor cells containing only GBT with GAD-CN1c (26) show a detectable signal above background. Two subunits of calcineurin (CNA1, CNB1) known to interact with each other are used as a positive control for the assay (20). The data presented in Figure 2A show that CN1c interacts specifically with CNA1 and CNA2, but not with G4BD or lamin C.

A similar set of experiments, illustrated in Fig. 3A, is conducted using constitutively-active CNA subunits, as well as calcineurin subunit CNB1. As described in the Materials and Methods section below, CNA1 Δ C and CNA2 Δ C are each missing a C-terminal portion of the protein containing an autoinhibitory domain. Exemplary results from these experiments are shown in Figure 3A. The legend for Fig. 3A is shown in Figure 3B. The data show that GBT-A1 Δ C and GAD-CN1c (28) gives a definite positive signal, while GBT-A2 Δ C and GAD-CN1c (29) is weaker, though still detectable above its background (*i.e.* GBT-A2 Δ C and GAD; 31). The signal from GBT-B1 and GAD-CN1c (32) is not detectable above vector background (GBT-B1 and GAD; 33). Positive controls GBT-A1 Δ C and GAD-B1 (34) and GBT-A2 Δ C and GAD-B1 (35) give strong signals. The data presented in Figure 3A show that CN1c interacts specifically with CNA1 Δ C and CNA2 Δ C, but not with CNB1.

Example 3 details the effects of immunosuppressant drugs on binding of CN1c to calcineurin in B1⁺, B1 Deletion and B1 Overproducing Yeast Strains. The yeast strains are assayed for β -gal activity as above to determine if the immunosuppressant drugs FK506, cyclosporin A (CsA) and rapamycin affect the binding of CN1c to subunits of calcineurin. The experiments are performed in yeast strains wild-type for the CNB1 subunit, null for the CNB1 subunit, and in yeast transformed with a high efficiency expression vector containing DNA encoding the CNB1 subunit.

Exemplary data are shown in Figures 4A, 4C, 5A and 5C. The legends for Figs. 4A and 4C are shown in Figures 4B and 4D, respectively. Figs. 4A and 5A illustrate experiment

performed without FK506, while experiments shown in Figs. 4C and 5C were performed with FK506.

The interactions of various combinations of proteins expressed by constructs indicated in Example 3 was studied in three yeast strains, one of which is null for the CNB1 subunit of calcineurin (Y153b; at 36-40), while the others (Y190; at 41-46 and Y526 at 47-51) are wild-type for CNA1, CNA2 and CNB1.

The data, shown in Fig. 4A (no added drugs), illustrate that deleting the endogenous host CNB1 gene potentiates, or enhances, interactions between CN1c and calcineurin subunits CNA1, CNA2, CNA1ΔC and CNA2ΔC. Comparison of corresponding colonies in Figs. 4A and 4C shows the effects of FK506 on CN1c-CNA/CNAΔC interactions. The drug enhances interactions under all except control conditions. The effect is most striking in yeast strains wild-type for the CNB1 subunit (*e.g.*, compare 50a with 50b, and 51a with 51b).

The drug also markedly enhances, or potentiates CN1c-CNA/CNAΔC interactions under conditions where the CNB1 subunit is overexpressed. Figure 5A shows the effect of overexpressing CNB1 on CN1c-CNA/CNAΔC interactions in the absence of drug. Colonies expressing B1/YEp352 (53a, 55a-58a) have reduced signal as compared with controls expressing only YEp352 (52a, 54a). Inclusion of FK506 in the plating medium (Fig. 5C), however, enhances, or potentiates interactions in all colonies, except the negative controls (56).

The data presented in Figures 4A, 4C, 5A and 5C demonstrate that the interaction of CN1c with CNA and CNAΔC is markedly enhanced by FK506. The interaction is also enhanced by deletion of CNB1 and diminished by overexpression of CNB1, and the inhibitory effect of CNB1 overproduction is overcome by the stimulatory effect of FK506.

Stated another way, inclusion of a small molecule immunosuppressant (FK506) potentiates an interaction between two fusion hybrid proteins, where one of the two proteins contains an (A) subunit of calcineurin, and the other protein contains a CNI polypeptide. The potentiation is particularly strong when the cell is further modified to cause overexpression of a "B" subunit of calcineurin by said cell (*e.g.*, the expresses B1/YEp352).

In the present case, a yeast cell is modified to cause overexpression of a "B" subunit of calcineurin (CNB1) by transforming the cell with B1/YEp352 (construction described below). A cell may be modified to cause overexpression of a "B" subunit of calcineurin in other ways as well, such as, for example, transformation with other types of expression vectors encoding a "B" subunit of calcineurin, or treatment with a substance that upregulates a promoter controlling expression of an endogenous (B) subunit of calcineurin.

In light of the effects of FK506 on CN1c-CNA/CNAΔC interactions, two other immunosuppressants, cyclosporin A and rapamycin, were examined in similar experiments. The results of these experiments are shown in Figures 6A-6F and 7A-7H.

The data presented in Figures 6A and 6C are essentially equivalent to those presented in Figures 4A and 4C, respectively. Data shown in Figure 6E demonstrate that like FK506, the immunosuppressant cyclosporin A is also effective to enhance interaction of CN1c with CNA and CNAΔC. Both FK506 and cyclosporin A are known to exert their immunosuppressive effects through calcineurin (Cyert).

Similarly, data shown in Figures 7A and 7C support data in Figures 5A and 5C, and further, demonstrate that there is no detectable interaction between FK506 binding protein (FKBP) and CN1c. Results shown in Fig. 7E demonstrate that cyclosporin A has a similar effect to FK506 in cells overexpressing CNB1 — that is, it enhances the interactions between CN1c and CNA/CNAΔC.

In contrast, data presented in Fig. 7G show that the immunosuppressant rapamycin has no detectable effect on CN1c-CNA/CNAΔC interactions (compare Fig. 7G with Fig. 7A).

Taken together, the data presented in Figs. 6A, 6C, 6E 7A, 7C, 7E and 7G show that like FK506, cyclosporin A (CsA), but not rapamycin, enhances the interaction of CN1c with CNA and CNAΔC, and that CN1c doesn't interact with FKBP with or without FK506.

Example 4 describes experiments to assess effects of CN1c on FKBP/FK506 binding to calcineurin. Figure 8A presents exemplary data from studies to assess the effect of CNI on FKBP-mediated FK506 interactions with CNA2. The legend for Fig. 8A is shown in Figure 8B. Data in Figure 8A demonstrate that, in the absence of FK506, FKBP and CNA2 show no detectable interaction (84). In the presence of FK506, however, the proteins interact (85), presumably because FK506 forms a complex with FKBP, which then binds CNA2 (Cyert).

Data in Figure 8A further show that, in the absence of FK506, CNI has no effect on the lack of interaction between FKBP and CNA2 (86). In the presence of FK506 (87), however, CNI potentiates, or enhances the binding between FKBP and CNA2 (compare the intensity at 87 with that at 85). This effect suggests that CNI and similar compounds may be employed to increase the sensitivity of calcineurin to immunosuppressant drugs that act on it, and in this way, decrease the amount of the immunosuppressant required for a particular level of immunosuppression.

Experiments illustrated in Figures 9A and 9B demonstrate that FK506 has little or no effect on the binding of CNA to CNB1. The legends for Fig. 9A and 9B are shown in Figures 9B and 9D, respectively. The data in Fig. 9A show that overexpression of the full-length CNI

clone markedly enhances the FK506-dependent interaction of FKBP with CNA, although it doesn't affect the interaction between CNA and CNB1.

Example 5 presents co-immunoprecipitation of CN1c (carrying an HA epitope tag) and CNA. Immunoprecipitation is carried out with anti-HA monoclonal antibody and the immune complex, resolved by SDS-PAGE, is detected with anti-CNA2 polyclonal antibody and visualized with goat anti-rabbit antibody using the "ECL" method (Amersham, Arlington Heights, IL). The results, shown in Figure 10, demonstrate that CN1c is capable of binding to CNA2 tightly enough for the complex to be co-immunoprecipitated. Similar methods may be employed to isolate a CNI analog from other cell sources, including mammalian (specifically human).

Example 6 describes yeast RNA blots hybridized with a CN1c probe. Exemplary data are shown in Figure 11. A single message of approximately 2.9 kb is detected. The data indicate that CNI is an expressed gene encoding a 2.9 kb message in yeast.

Example 8 details the construction of *cni* null mutants. The null mutants are employed to assess if *CNI* is required for viability in yeast, and to test hygromycin B sensitivity. The experiments indicate that CNI is not essential for viability, since CNI deletion mutant strains can survive, but that CNI deletions render a host more resistant to hygromycin B. The effect is particularly pronounced in both MCY300-1 (*cna1⁻cna2⁻*) and DD12 (*cnb1⁻*), suggesting that CNI functions as a suppressor of CN mutant's sensitivity to hygromycin B.

It will be understood that all of the above methods and experimental manipulations are amenable to being done with interacting polypeptides from organisms other than yeast. In particular, calcineurin subunits, CNI polypeptides, immunophilins and the like may be of mammalian origin, *e.g.*, human origin.

VII. UTILITY

Methods and compositions of the present invention may be applied in a number of different ways. Following the guidance presented herein, one of skill in the art may isolate nucleic acids encoding additional CNI polypeptides, for example, a human CNI polypeptide.

In one approach, a yeast strain carrying a mutation of the *CNI* gene, *e.g.*, a deletion, is used to clone heterologous sequences (*e.g.*, human sequences) by complementation. A library of genomic DNA or, preferably, cDNA from an organism (*e.g.*, human) and tissue (*e.g.*, lymphocyte cells) of choice is cloned into a vector that can be maintained in yeast. Preferably, the vector contains a yeast promoter effective to express the heterologous sequences in yeast cells. Several heterologous libraries suitable for expression in *Saccharomyces*

cerevisiae containing DNA from *S. pombe* (Beach, *et al.*) and *Drosophila* have been constructed.

The library is transformed into a suitable yeast strain carrying a *cni* mutation, and transformants are selected using a suitable complementation assay. For example, transformants
5 may be screened for increased hygromycin sensitivity, as experiments described herein indicate that *cni* deletion mutants possess a decreased sensitivity to hygromycin B (Example 8). The screen may be made more effective by using a yeast strain that is hypersensitive to hygromycin B, such as a strain deficient for a subunit of calcineurin (Example 8).

Alternatively, human CNI DNA sequences may be isolated by directly screening a
10 library, *e.g.*, a lymphocyte cDNA library, for clones hybridizing with a yeast CNI nucleic acid probe. The generation of an exemplary yeast CNI nucleic acid probe is described in Example 1.

In another approach, particularly advantageous for isolating sequences expressed at low levels, a CNI nucleic acid probe may be used to screen a genomic library, *e.g.*, a human
15 genomic library, to isolate a sequence that may be used to design probes or primers that may match the target sequence better than the yeast sequence. Such primers may be used with, for example, PCR, to isolate longer fragments from a tissue-specific library.

In yet another approach, an antibody generated against CNI polypeptide is used to immunoprecipitate a CNI polypeptide from an organism and/or tissue of choice. The protein
20 may then be micro-sequenced, and the sequence utilized to design degenerate primers useful for isolating a cDNA.

CNI polypeptides of the present invention, particularly CNI fragments that retain a desired binding activity, may be used as lead compounds useful for the development of small molecules having cellular functions similar to those of the CNI-polypeptides, that is, molecules
25 effective to enhance immunosuppressive effects of calcineurin-targeted immunosuppressants by potentiating an interaction of an immunophilin with calcineurin.

CNI-polypeptides of the present invention may also be employed in a method of increasing sensitivity of cells to calcineurin-affecting immunosuppressant drugs. In this method, a CNI-polypeptide is introduced into the cell typically prior to or at the same time as
30 contacting the cell with an immunosuppressant drug, such as FK506. The polypeptide may be delivered by any suitable means effective to deliver polypeptides to selected cells.

Alternatively, nucleic acids encoding CNI polypeptides may be used in appropriate expression vectors as a genetic therapy tool to potentiate the immunosuppressive effects of

calcineurin-targeting immunosuppressant drugs. The vectors may be targeted to selected cells, such as T-cells, to increase their sensitivity to a given systemic dose of an immunosuppressant.

Another utility of the present invention includes methods of screening for substances that up-regulate expression of CNI polypeptides, *i.e.*, substances that affect transcription. Such substances are useful for sensitizing cells to immunosuppressant drugs. In this method, the CNI promoter can be attached to a gene that functions as a selectable marker (for use in genetic selections to screen test substances) or to a reporter gene (for use in evaluating the effect on CNI transcription by test substances).

In another aspect of the present invention, the CNI-polypeptides, for example, mammalian homologue polypeptides of CNI, have potential use as therapeutic agents for both human and veterinary use. For example, CNI-polypeptides may be used in a method of enhancing immunosuppression in a test subject. In this method, the CNI-polypeptide is administered to the subject in a pharmaceutically-acceptable formulation and at a concentration effective to potentiate the interaction of an immunosuppressant/immunophilin complex with a subunit of calcineurin. The method may also include contacting the CNI-polypeptide with a cell under conditions effective to permit uptake of the protein into the cell in order to increase sensitivity of the cell to immunosuppressants. A CNI polypeptide used in such methods may be modified to be more suitable for administration or to be more effective in a cell. For example, a CNI polypeptide may be modified to eliminate PEST motifs, which are typically found in proteins with short half-lives, to extend the effective lifetime of the polypeptide in the target cell.

The following examples illustrate, but in no way are intended to limit the present invention.

25

MATERIALS AND METHODS

Unless indicated otherwise, chemicals and reagents were obtained from Sigma Chemical Company (St. Louis, MO) or Mallinckrodt Specialty Chemicals (Chesterfield, MO), restriction endonucleases were obtained from New England Biolabs (Beverly, MA), and other modifying enzymes and biochemicals were obtained from Pharmacia Biotech (Piscataway, NJ) or Boehringer Mannheim (Indianapolis, IN). FK506 was obtained from Fujisawa USA, Inc. (Deerfield, IL), cyclosporin A was obtained from Sandoz (Basel, Switzerland), and rapamycin was obtained from Wyeth-Ayerst (Princeton, NJ). Materials for media for yeast growth and culture were obtained from DIFCO (Detroit, MI). Unless otherwise indicated, manipulations

of yeast, bacteria, nucleic acids, proteins and antibodies were performed using standard methods and protocols (e.g., Guthrie, *et al.*, Sambrook, *et al.*, Ausubel, *et al.*, Harlow, *et al.*, and Rose, *et al.*).

5 A. Buffers

Z buffer: 60 mM Na₂HPO₄·7H₂O, 40 mM NaH₂PO₄·H₂O, 10 mM KCl, 1 mM MgSO₄·7H₂O and 50 mM β-mercaptoethanol (pH 7.0).

 B. Plasmids, Libraries and Yeast Strains

10 Plasmids pGBT9 (GBT), carrying GAL4 DNA-binding domain (amino acid residues 1-147; G4BD) and TRP1, and pGAD (GAD), carrying GAL4 activation domain (amino acid residues 768-881; G4AD) and LEU2; three pGAD libraries carrying fusions between G4AD and yeast genomic *Sau3AI* partial-digest fragments in each frame; and the yeast *GAL1-lacZ* reporter strain SFY526 (Y526; *MATa ura3-52 ade2-101 lys2-801 his3-200 trp1-901 leu2-3,112*
15 *can1 gal4-542 gal80-538 URA3::GAL1-lacZ*) were obtained from Stanley Fields (State University of New York at Stony Brook, Stony Brook, NY; Chien, *et al.*, Bartel, *et al.*). The libraries were constructed with linkers between the GAL4 activation domain and the *Sau3AI* fragments. The sequences of the linkers were 5'-ATCG-3' for the first library, 5'-ATCCG-3' for the second library, and 5'-ATCCCG-3' for the third library. In this way, the yeast
20 genomic *Sau3AI* fragments were cloned in all three reading frames relative to G4AD.

 Plasmids pAS2 (AS) carrying G4BD and TRP1, and pAS-lamin (AS-lamin) containing a sequence encoding a G4BD-lamin C fusion; and yeast reporter strains Y190 (*MATa ura3-52 ade2-101 his3-Δ200 trp1-901 leu2-3,112 cyh2Δ, gal4Δ gal80Δ URA3::GAL-lacZ LYS2::GAL-HIS3*), a derivative of Y153 carrying dual indicator genes (GAL-lacZ and GAL-
25 HIS3), and Y187 (*MATa ura3-52 ade2-101 lys2-801 his3-200 trp1-901 leu2-3,112 gal4Δ gal80Δ URA3::GAL-lacZ*) carrying *GAL-lacZ* reporter were obtained from Stephen Elledge (Baylor College of Medicine, Houston, TX; Durfee, *et al.*). Yeast strain Y153b1 (*cnb1::ADE2*) was derived from Y153.

E coli strain JBe181 (leuB600 trpC9830) was obtained from Ira Herskowitz (University
30 of California at San Francisco, San Francisco, CA). Protease-deficient yeast strain BJ2407 (Guthrie, *et al.*) was obtained from the Yeast Genetic Center (University of California at Berkeley, Berkeley, CA).

C. GAL4-Calcineurin Fusions

GAL4-calcineurin (GAL4-CN) fusions, GBT-A1 (G4BD-CNA1), GBT-A2 (G4BD-CNA2), GBT-B1 (G4BD-CNB1), GAD-A1 (G4AD-CNA1), GAD-A2 (G4AD-CNA2), and GAD-B1 (G4AD-CNB1) were constructed as follows. Plasmids containing inserts encoding
5 CN subunits CNA1 (SEQ ID NO:9; Cyert, *et al.*, 1991), CNA2 (SEQ ID NO:11; Cyert, *et al.*, 1991) and CNB1 (SEQ ID NO:13; Cyert, *et al.*, 1992) were subjected to site-directed mutagenesis (Kunkle) to introduce a *Bam*HI site just upstream of each subunit's initiation codon in the second reading frame. DNA prepared from the mutated plasmids was digested with *Bam*HI and *Xho*I, and the resulting *Bam*HI-*Xho*I fragments, each containing a full-length coding
10 sequence, were cloned into GBT or GAD that had been cut with *Bam*HI and *Sal* I. The resulting plasmids encoded in-frame fusions of the CN subunits with G4BD or G4AD.

Plasmids encoding CNA protein variants with truncated C-termini (GBT-A1ΔC, GBT-A2ΔC) were constructed by introducing stop codons after amino acid residues 509 (CNA1) and 502 (CNA2). The 44-residue deletion in GBT-A1ΔC removed the autoinhibitory domain of
15 CNA1, while the 102-residue deletion in GBT-A2ΔC removed both the autoinhibitory and the calmodulin-binding domains of CNA2 (Cyert, *et al.*, 1991).

Plasmid GBT-FKBP, containing an FK506 binding protein (FKBP) gene fused to the GAL4 binding domain, was constructed by introducing a *Bgl*II site upstream of the initiation codon and a *Bam*HI site downstream of the stop codon of FKBP12 (Heitman, *et al.*) and
20 ligating the *Bgl*II-*Bam*HI fragment into GBT cut with *Bam*HI.

Plasmid B1/YEp352 was constructed to contain the full coding sequence of CNB1 (SEQ ID NO:13, Cyert, *et al.*, 1992) as a 1.4 kb *Bam*HI-*Eco*RI fragment encompassing the sequence presented as SEQ ID NO:13 (812 bp; contains the coding sequence), in the multicopy plasmid YEp352(HIS), which is derived from YEp352 (URA) (Hill, *et al.*).

25 Plasmid CNI/YEp352(HIS) (also referred to as CNIH) was constructed by ligating a 3.16 kb *Mun*I-*Eco*RV fragment, containing the full coding sequence of CNI, from plasmid CNI7.1 (construction described below) into YEp352(HIS) cut with *Eco*RI and *Sma*I. Plasmids CNI/YEp352(TRP) (also referred to as CNIT) and CNI/YEp352(URA) (also referred to as CNIU) were similarly constructed using the 3.16 kb fragment and YEp352(TRP) or
30 YEp352(URA), respectively (Hill, *et al.*).

Plasmids A1/YEp351 and A2/YEp352 were constructed to contain the full coding sequences of CNA1 (SEQ ID NO:9, Cyert, *et al.*, 1991) in YEp351 (Hill, *et al.*) and CNA2 (SEQ ID NO:11, Cyert, *et al.*, 1991) in YEp351 and YEp352, respectively. A1/YEp351 was constructed by ligating a 2.9 kb *Sac*I-*Hind*III fragment from clone CNA1 (Cyert, *et al.*, 1991)

into YEp351(HIS) cut with *SacI* and *HindIII*. A2/YEp352 was similarly constructed by ligating a 3 kb *SpeI-HindIII* fragment from clone CNA2 (Cyert, *et al.*, 1991) into YEp352(HIS) cut with *XbaI* and *HindIII*.

5 All GAL4-CN fusions were verified by DNA sequencing (Sanger, *et al.*) using "SEQUENASE 2.0" sequencing kits (United States Biochemical, Cleveland, OH), and were subjected to the following tests. The functionality of the fusion proteins was assayed by determining whether they could complement the appropriate *cn⁻* mutant phenotypes, using assays to measure the sensitivity to pheromone and Mn^{2+} (Reneke, *et al.*, Cyert, *et al.*, 1991). All of the GAL4-CN fusions were functional in this assay.

10 The fusion proteins were also tested for their ability to activate the reporter gene in the absence of the complementary GAL-4 domain fusion (*i.e.*, in the presence of the complementary GAL4 domain not fused to a second protein, for example, G4BD-A1 vs G4AD) using the two-hybrid interaction assay described below. Only GBT-B1 and GAD-A1 were able to activate the reporter gene at low levels without the complimentary GAL-4 domain fusion –
15 assays with the other fusion proteins in the absence of the complimentary GAL-4 domain fusion showed no detectable levels of expression.

The two-hybrid interaction assay was also used to test the ability of the fusions to interact specifically with another fusion containing complimentary GAL4 and CN domains (*e.g.*, G4BD-A1 interacting with G4AD-B1). All CN hybrids were able to react specifically
20 and result in an activation of the reporter gene that was clearly detectable above background. The high specificity witnessed in these experiments indicates that the GAL4 two-hybrid system can reliably be used to assay interactions between CN and other proteins.

D. Yeast GAL4 Two-Hybrid System for Detecting Protein-Protein Interaction

25 In the library screen, described in more detail in Example 1A, the yeast strain Y190, harboring the hybrid plasmid carrying the GAL4 binding domain fused to the A1 subunit of calcineurin (G4BD-CNA1), was transformed with fusion libraries carrying yeast genomic DNA *Sau3AI* fragments fused to the GAL4 activation domain. Transformants that were able to express the reporter genes, *i.e.*, able to grow on -His + 3-AT and to score blue in β -gal assay,
30 were selected as candidate positives. These candidate positives potentially contain library DNA fragments encoding proteins that physically interact with CNA1.

In another application described herein, the two-hybrid system was used to test for interactions between CNA (fused to one of the GAL4 domains) and CNB1 (fused to the other GAL4 domain), and between CNA and FKBP. Additional experiments tested a clone, CN1c,

isolated using the library screen, against a series of proteins fused to the complementary GAL4 domain under various conditions to test whether CN1c interacts with CNA subunits, and if so, how the interactions are affected by various conditions.

5 E. Color Development (β -gal) Assay

Yeast reporters harboring both G4BD and G4AD fusions (and a third non-fusion plasmid in some cases) were monitored for β -gal activity as follows. Purified yeast transformants were patched onto selective plates with or without other test reagents. After growing 3 days at 30°C, colonies were lifted onto nitrocellulose filters, permeabilized in liquid
10 nitrogen as above, placed on Whatman No. 1 paper in petri dishes containing 0.1% X-Gal in Z buffer (see above), and incubated at 30°C for 12 hours. Blue color begins to appear in positive colonies between about one half and ten hours into the incubation period.

Exemplary images obtained using the color development assay are presented in Figures 2A, 3A, 4A, 4C, 5A, 5C, 6A, 6C, 6F, 7A, 7C, 7E, 7G, 8A, 9A and 9C.

15

F. Growth Assay

A growth assay, applicable to yeast strains Y190 and Y153b1 which carry both *GAL-HIS3* and *GAL-lacZ* reporters, was sometimes used as a complement to the color assay described above. Yeast transformants were streaked onto selective plates containing 40-50 mM
20 3-AT and no Histidine, and incubated at 30°C for 3-7 days. Growth (corresponding to the level of *HIS3* expression) was monitored as an indicator of the interaction between fusion proteins. In cases where both assays were used, the amount of cell growth typically correlated well with the color intensity in the β -gal assay.

25 G. Yeast Growth, Drug Treatment

Yeast were typically grown in YPD (rich non-selective) or synthetic complete (SC) medium with selected component drop-outs, depending on the plasmid introduced, following standard procedures (Sherman, *et al.*, Ausubel, *et al.*).

Experiments utilizing treatment with drugs or additives were performed by including
30 the drug or additive in the medium. For plating, the agar was autoclaved, allowed to cool to 50°C, and the drug or additive was added before pouring the plates. Unless otherwise indicated, drugs and additives were added to result in the following final medium concentrations: FK506: 1 μ g/ml, cyclosporin A: 10 μ g/ml, rapamycin: 10 ng/ml, and hygromycin B: 40 μ g/ml.

H. Antibodies

Polyclonal and monoclonal antibodies, for use in the present invention, can be prepared by standard methods (Harlow, *et al.*) utilizing the CNI polypeptides of the present invention, for example, a substantially purified CNI/ β -galactosidase fusion protein (Example 9).
5 Antibodies can also be generated by recombinant techniques (Cabilly, *et al.*; Better, *et al.*; Skerra, *et al.*). In addition to whole antibody molecules, antibody fragments retaining the immunological specificity of the whole antibody may also be used in the practice of the present invention (e.g., Fab and F(ab')₂ fragments of IgG (Pierce Chemical, Rockford, IL)). The antibodies can be purified by standard methods to provide antibody preparations which are
10 substantially free of serum proteins that may affect reactivity (e.g., affinity purification (Harlow *et al.*)).

EXAMPLE I

Isolation of CN1c

15 A. Library Screening

Yeast strain Y190 was transformed with pGBT-CNA1 *TRP1* (GBT-A1) hybrid plasmid using the transformation protocol described by Schiestl, *et al.* Transformants were selected, colony purified, and a single transformant was selected to make (Y190 GBT-A1)-competent cells, following the procedure described in Guthrie, *et al.*.

20 The three pGAD yeast fusion libraries described above, carrying fusions between G4AD and yeast genomic DNA *Sau3A*I fragments in each reading frame, were then used to transform (Schiestl, *et al.*) the Y190 GBT-A1-containing cells. Transformants were plated onto SC-Trp-Leu-His plates containing 40 mM 3-aminotriazole (3-AT; Sigma Chemical Co., St. Louis, MO) and incubated at 30°C for 6 days to screen for HIS⁺ colonies (Durfee, *et al.*).

25 His⁺ colonies were replica plated onto nitrocellulose filters (Schleicher & Schuell, Keene, NH), frozen in liquid nitrogen for approximately 30 seconds, and incubated at 30°C for 12 hours with Z buffer (see above) containing the chromogenic substrate X-Gal (0.1%) to assay β -gal activity (Breedon, *et al.*).

Candidate positive (blue) colonies were re-streaked for single colonies. Single colonies
30 were purified and retested using the above protocol. Colonies which reproducibly tested positive were screened using PCR with primers directed against the internal portion of GAL-4 (i.e. the portion between the DNA binding domain and the activation domain). The sequences of the primers, G4-PCR-A and G4-PCR-B, are given as SEQ ID NO:22 and SEQ ID NO:23,

respectively. Colonies yielding a PCR product were identified as containing intact GAL4, and were eliminated.

The GBT-A1 *TRP*⁺ plasmid was eliminated by growing in *Trp*⁺ liquid media for 2-3 days, plating on -Leu media and then replica-plating on -Leu and -Trp plates to identify and
5 eliminate colonies that had lost the GBT-A1 plasmid, yet still gave a positive signal.

Plasmid DNA was extracted from the remaining *Leu*⁺ candidates. The plasmid DNA was transformed into *E coli* JBe181 and plated on -Leu media to select for library plasmids. The library plasmids isolated by this method were introduced back to the yeast reporter strains either alone or with test G4BD fusions: GBT, GBT-A1, and AS-lamin.

10 A parallel specificity assay was conducted by mating. Candidate strains, as described above, were 3-AT growth positive and X-gal positive when both the library and GBT-A1 plasmids were present. After elimination of the GBT-A1 plasmid from these strains, strains that were *Leu*⁺ *Trp*⁻ 3-AT growth⁻ and β -gal⁻ were mated to the following strains: Y187 (*MAT α*) carrying GBT, GBT-A1, or AS-lamin, and the diploids were assayed.

15 Among the 3-AT positive, β -gal positive candidates identified by the secondary screening method just described, one clone (III-21S, later termed GAD-CN1c) was specifically positive in conjunction with GBT-A1 in both the transformation assay and the mating assay.

B. Sequence of CN1c

20 Clone III-21S was sequenced as above. The sequence is presented herein as SEQ ID NO:1, and a schematic representation of the clone is shown in Figure 1A. The *Sau3AI* library insert encodes 306 amino acids followed by a stop codon in frame with the coding sequence of GAL4, but does not contain an in-frame ATG start site upstream of the stop codon. This is consistent with the fragment encoding a c-terminal portion of a complete gene product.
25 Accordingly, the clone was termed CN1c, with the lowercase "c" representing "c-terminal".

The stippled portion between GAL-4AD and CN1c in Figure 1A represents the linker discussed in Materials and Methods, above. Also indicated in the Figure are the approximate locations of in-frame start (ATG) and stop codons, and *Sau3AI* restriction sites.

30 C. Isolation of a Full Length Clone

A ³²P-labeled CN1c probe was generated from the 1.22 kb CN1c insert of clone III-21S by polymerase chain reaction (PCR) using primers represented as SEQ ID NO:7 and SEQ ID NO:8. The probe was used to map the gene to the right arm of chromosome 11 by hybridization screening (Sambrook, *et al.*) a panel of λ clones (American Type Culture

Collection (ATCC), Rockville, MD) spanning the entire yeast genome. Two clones, 70500 and 70590, gave positive hybridization signals. A phage lysate of clone 70500 in λ MG3 was obtained from the ATCC, was amplified, purified, restriction-mapped and used as a DNA source for subsequent cloning experiments.

- 5 The phage DNA was digested with *SacI*, yielding a 7.1 kb fragment containing the entire CNI gene. This fragment was cloned into "BLUESCRIPT SK-" (Stratagene, La Jolla, CA) cut with *SacI*, yielding plasmid CNI7.1. Plasmid CNI7.1 was digested with *MunI* and *EcoRV*, releasing a 3.16 kb fragment containing the entire coding sequence of CNI. The 3.16 kb fragment was then cloned into each of YEp352(HIS), YEp352(TRP), YEp352(URA), and
- 10 "BLUESCRIPT SK-", each cut with *EcoRI* and *SmaI*, yielding plasmids CNIH, CNIT, CNIU and CNI3.2, respectively. The sequence of the 3.16 kb *MunI/EcoRV* fragment is encompassed by the 3.5 kb sequence presented as SEQ ID NO:4. The *MunI* site is at nucleotide 100 of SEQ ID NO:4, and the *EcoRV* site is at nucleotide 3263 of SEQ ID NO:4.

- A schematic diagram of the sequence presented as SEQ ID NO:4 is shown in Figure
- 15 1B. This sequence contains the 3.16 kb *MunI/EcoRV* fragment used in many of the experiments described herein (depicted in Figure 1B as the portion between the *MunI* and *EcoRV* sites), which contains the entire 2.75 kb coding sequence of CNI (SEQ ID NO:6; graphically indicated in Figure 1B by the locations of the "ATG" and "Stop" codons).

- Figure 13 also shows the location of certain features of the sequence. For example,
- 20 "PEST" motifs (Rogers, *et al.*, Dice) are indicated by bars over the corresponding sequence.

A search of known DNA and protein sequences turned up no obvious matches or homologies to genes in other organisms. Accordingly, CNI may represent a new type of calcineurin-binding protein.

25

EXAMPLE 2

Binding of CNIC to Calcineurin

Y190 yeast carrying the plasmids indicated below were assayed for β -gal activity by color development assay described above to determine the specificity of binding of CNIC to subunits of calcineurin.

- 30 Exemplary data, in the form of images of filters having yeast colony replicas that had undergone the β -gal color development assay are shown in Figure 2A. The legend for Fig. 2A is shown in Figure 2B. Numbers in the legend refer to locations of yeast colonies expressing particular combinations of plasmid constructs. The constructs are as follows: 20:GBT-A1 and

GAD-B1, 21:GBT-A1 and GAD-CN1c, 22:GBT-A1 and GAD-CN1c, 23:GBT-A1 and GAD-CN1c 24:GBT-A2 and GAD-CN1c 25:AS-lamin and GAD-CN1c 26:GBT and GAD-CN1c.

Yeast colonies used in the assay were derived by several different methods. Those at location 22 were purified colonies from the original library screen, those at 21 were colonies transformed with mini-prep DNA of the isolated GAD-CN1c plasmid, and the remaining colonies (23, 24, 25 and 26) were transformed with maxi-prep (Qiagen, Chatsworth, CA) DNA of GAD-CN1c.

A comparison of the intensities of the blue β -gal reaction product indicates that CN1c interacted strongly with CNA1 regardless of the source of the CN1c plasmid DNA (20, 21, 22 and 23), and somewhat less strongly with CNA2 (24). Neither cells containing AS-lamin with GAD-CN1c (25), nor cells containing only GBT with GAD-CN1c (26) showed a detectable signal above background. Two subunits of calcineurin (CNA1, CNB1) known to interact were used as a positive control for the assay (20).

In summary, the data above show that CN1c interacted specifically with CNA1 and CNA2, but not with G4BD or lamin C.

A similar set of experiments was conducted using constitutively-active CNA subunits, as well as calcineurin subunit CNB1. As described in Materials and Methods, above, CNA1 Δ C and CNA2 Δ C were each missing a C-terminal portion of the protein containing an autoinhibitory domain. Exemplary results from these experiments are shown in Figure 3A. The legend for Fig. 3A is shown in Figure 3B. Locations of yeast colonies expressing specific constructs are as follows: 27:GBT and GAD-CN1c, 28:GBT-A1 Δ C and GAD-CN1c, 29:GBT-A2 Δ C and GAD-CN1c, 30:GBT-A1 Δ C and GAD, 31:GBT-A2 Δ C and GAD, 32:GBT-B1 and GAD-CN1c, 33:GBT-B1 and GAD, 34:GBT-A1 Δ C and GAD-B1, and 35:GBT-A2 Δ C and GAD-B1.

The data show that GBT-A1 Δ C and GAD-CN1c (28) gave a definite positive signal, while GBT-A2 Δ C and GAD-CN1c (29) was weaker, though still detectable above its background (*i.e.* GBT-A2 Δ C and GAD; 31). The signal from GBT-B1 and GAD-CN1c (32) was not detectable above vector background (GBT-B1 and GAD; 33). Positive controls GBT-A1 Δ C and GAD-B1 (34) and GBT-A2 Δ C and GAD-B1 (35) gave strong signals.

These data show that CN1c interacted specifically with CNA1 Δ C and CNA2 Δ C, but not with CNB1.

EXAMPLE 3**Effects of Immunosuppressant Drugs on Binding of CN1c to Calcineurin in B1⁻, B1
Deletion and B1 Overproducing Yeast Strains**

Three yeast strains carrying the plasmids indicated below were assayed for β -gal
5 activity as above to determine if the immunosuppressant drugs FK506, cyclosporin A (CsA)
and rapamycin affect the binding of CN1c to subunits of calcineurin. The experiments were
performed in yeast strains wild-type for the CNB1 subunit, null for the CNB1 subunit, and in
yeast transformed with a high efficiency expression vector containing DNA encoding the CNB1
subunit.

10 Exemplary data, in the form of filter images produced as above are shown in Figures
4A, 4C, 5A and 5C. Plates used to make the filters shown in Figs. 4A and 4C were replicas
from one master plate, while plates used to make the filters shown in Figs. 5A and 5C were
replicas from another plate. The plates used to generate filters shown in Figs. 4A and 5A were
without FK506, while the plates used to generate filters shown in Figs. 4C and 5C contained
15 1 μ g/ml FK506.

The legends for Figs. 4A and 4C are shown in Figures 4B and 4D, respectively. Since
the imaged filters in Figs. 4A and 4C were from replica plates, corresponding locations on each
filter contain material from the same yeast colonies. Accordingly, the locations are referred
to by the same "base" numbers in the legends. To facilitate reference to a specific location on
20 a specific filter, the base numbers are followed by a lowercase letter that is different for each
of the individual filters. For example, in the present figure, "a" follows the base numbers to
identify locations on the filter shown in Fig. 4A, while a "b" follows the base numbers to
identify locations on the plate in Fig. 4C. This labeling scheme is used in other experiments
detailed herein where multiple filter lifts are shown.

25 The interactions of various combinations of proteins expressed by constructs indicated
below was studied in three yeast strains. Strain Y153b, at 36-40, is null for the CNB1 subunit
of calcineurin. Strains Y190 (41-46) and Y526 (47-51) are wild-type for CNA1, CNA2 and
CNB1.

Hybrid proteins expressed by colonies at specific locations are as follows: 36:GBT-A1 and
30 GAD-CN1c, 37:GBT-A2 and GAD-CN1c, 38:GBT-A1 Δ C and GAD-CN1c, 39:GBT and GAD-
CN1c, 40:GBT-A2 Δ C and GAD-CN1c, 41:GBT-A1 and GAD-CN1c, 42:GBT and GAD-CN1c,
43:GBT-A2 and GAD-CN1c, 44:GBT-A1 Δ C and GAD-CN1c, 45:GBT-A1 and GAD-B1,
46:GBT-A2 Δ C and GAD-CN1c, 47:GBT-A1 and GAD-CN1c, 48:GBT and GAD-CN1c,

49:GBT-A2 and GAD-CNlc, 50:GBT-A1ΔC and GAD-CNlc, and 51:GBT-A2ΔC and GAD-CNlc.

Yeast strain Y526 was used for all experiments shown in Figs. 5A, 5B, 5C and 5D. The expression vector B1/YEp352(HIS) was not used in strains Y190 or Y153b1 because they
5 are HIS⁺ in the absence of 3-AT.

The base numbers in Figures 5B and 5D correspond to locations of colonies expressing the following constructs: 52:GBT-A1, GAD-CNlc and YEp352, 53:GBT-A1, GAD-CNlc and B1/YEp352, 54:GBT-A2, GAD-CNlc and YEp352, 55:GBT-A2, GAD-CNlc and B1/YEp352, 56:GBT, GAD-CNlc and B1/YEp352, 57:GBT-A1ΔC, GAD-CNlc and B1/YEp352, and
10 58:GBT-A2ΔC, GAD-CNlc and B1/YEp352.

A comparison of data shown in Fig. 4A (no added drugs) shows the effect of deleting the endogenous host CNB1 gene on interactions between CNlc and calcineurin subunits CNA1, CNA2, CNA1ΔC and CNA2ΔC. Note that interactions in panels 36a-40a (CNB1 null strain) were all stronger (with the exception of the negative control in 39) than interactions in
15 corresponding panels 41a-51a (strains wild-type for CNB1). This result indicates that interaction between CNlc and CNA subunits were enhanced by the deletion of the CNB1 subunit.

Comparison of corresponding panels in Figs. 4A and 4C shows the effects of FK506 on CNlc-CNA/CNAΔC interactions. The drug enhanced interactions under all except control
20 (39, 42 and 48) conditions. The effect was most striking in yeast strains wild-type for the CNB1 subunit (*e.g.*, compare 50a with 50b, and 51a with 51b).

The drug also markedly enhanced CNlc-CNA/CNAΔC interactions under conditions where the CNB1 subunit was overexpressed. Figure 5A shows the effect of overexpressing CNB1 on CNlc-CNA/CNAΔC interactions in the absence of drug. Colonies expressing
25 B1/YEp352 (53a, 55a-58a) had reduced signal as compared with controls expressing only YEp352 (52a, 54a). Inclusion of FK506 in the plating medium (Fig. 5C), however, enhanced interactions in all colonies, except the negative controls (56).

Taken together, the above data demonstrate that the interaction of CNlc with CNA and CNAΔC was markedly enhanced by FK506. The interaction was also enhanced by deletion
30 of CNB1 and diminished by overexpression of CNB1, and the inhibitory effect of CNB1 overproduction was overcome by the stimulatory effect of FK506.

In light of the effects of FK506 on CNlc-CNA/CNAΔC interactions, two other immunosuppressants, cyclosporin A and rapamycin, were examined in similar experiments. The results of these experiments are shown in Figures 6A-6F and 7A-7H. Filters shown in

Figs. 6A-6F were from replica plates, as were those in Figs. 7A-7H. Colonies shown in Figs. 6A and 7A were plated without drugs; those in Figs. 6C and 7C were plated with FK506 (1 μ g/ml), those in Figs. 6E and 7E with CsA (10 μ g/ml), and those in Fig. 7G with rapamycin (10 ng/ml). Yeast strains used were as follows: In Figs. 6A-6F, panels 59-63 were Y153b1, 64-69 were Y190, and 70-74 were Y526. In Figs. 7A-7H, panels 77-83 were Y526, and panels 75 and 76 were Y190.

The base numbers in Figures 6B, 6D and 6F correspond to locations of colonies expressing the following constructs: 59:GBT-A1 and GAD-CN1c, 60:GBT-A2 and GAD-CN1c, 61:GBT-A1 Δ C and GAD-CN1c, 62:GBT and GAD-CN1c, 63:GBT-A2 Δ C and GAD-CN1c, 64:GBT-A1 and GAD-CN1c, 65:GBT and GAD-CN1c, 66:GBT-A2 and GAD-CN1c, 67:GBT-A1 Δ C and GAD-CN1c, 68:GBT-A1 and GAD-B1, 69:GBT-A2 Δ C and GAD-CN1c, 70:GBT-A1 and GAD-CN1c, 71:GBT and GAD-CN1c, 72:GBT-A2 and GAD-CN1c, 73:GBT-A1 Δ C and GAD-CN1c, and 74:GBT-A2 Δ C and GAD-CN1c.

The base numbers in Figures 7B, 7D, 7F and 7H correspond to locations of colonies expressing the following constructs: 75:GBT-FKBP and GAD, 76:GBT-FKBP and GAD-CN1c, 77:GBT-A1, GAD-CN1c and YEp352, 78:GBT-A1, GAD-CN1c and B1/YEp352, 79:GBT-A2, GAD-CN1c and YEp352, 80:GBT-A2, GAD-CN1c and B1/YEp352, 81:GBT, GAD-CN1c and B1/YEp352, 82:GBT-A1 Δ C, GAD-CN1c and B1/YEp352, and 83:GBT-A2 Δ C, GAD-CN1c and B1/YEp352.

The data presented in Figures 6A and 6C are essentially equivalent to those presented in Figures 4A and 4C, respectively. The constructs and yeast strains at corresponding locations were the same. As expected, the β -gal signal was also essentially equivalent between the two sets. Data shown in Figure 6E demonstrate that like FK506, the immunosuppressant cyclosporin A was also effective in enhancing interaction of CN1c with CNA and CNA Δ C. Both FK506 and cyclosporin A are known to exert their immunosuppressive effects through inhibition of calcineurin activity (Cyert).

Similarly, data shown in Figures 7A and 7C are essentially equivalent to those in Figures 5A and 5C, except that a top panel has been added in Figs. 7A-H. As above, the corresponding panels show the same constructs and yeast strains. The added panels (75 and 76) assessed the interaction of an FK506 binding protein (FKBP) with CN1c, and indicate that there were no detectable interactions between these proteins. Results in Fig. 7E demonstrate that cyclosporin A had a similar effect to FK506 in cells overexpressing CNB1 -- that is, it enhanced the interactions between CN1c and CNA/CNA Δ C.

In contrast, data presented in Fig. 7G show that the immunosuppressant rapamycin, which is known not to target calcineurin, had no detectable effect on CN1c-CNA/CNAΔC interactions (compare Fig. 7G with Fig. 7A).

Taken together, the above data show that like FK506, cyclosporin A (CsA), but not rapamycin, also enhanced the interaction of CN1c with CNA and CNAΔC. CN1c didn't interact with FKBP with or without FK506.

EXAMPLE 4

Effects of CNI on FKBP/FK506 binding to Calcineurin

Y526 cells, carrying the plasmids indicated below, were grown in -Trp-Leu-His liquid media with or without FK506 (1 μg/ml) until OD₆₀₀ reached about 1.0. Approximately the same number of cells, calculated based on OD₆₀₀ and equivalent to 1 ml of an OD₆₀₀=1 suspension, was harvested from each culture, washed once with ddH₂O, centrifuged briefly, and the pellet was resuspended in 30 μl ddH₂O and transferred onto a nitrocellulose filter. The filters were frozen in liquid nitrogen as described above, placed in a 8.5 cm petri dish containing a sheet of Whatman No. 1 paper (Whatman International LTD, Maidstone, UK) in 1.6 ml Z buffer containing 0.1% X-Gal, and incubated at 30°C for 8 hours.

Figure 8A presents exemplary data from studies to assess the effect of CNI overexpression on FK506-mediated FKBP interactions with CNA2. The legend for Fig. 8A is shown in Figure 8B. Locations of yeast colonies expressing specific constructs: 84:GBT-FKBP, GAD-A2 and YEp352, 85:GBT-FKBP, GAD-A2 and YEp352, 86:GBT-FKBP, GAD-A2 and CNI/YEp352, and 87:GBT-FKBP, GAD-A2 and CNI/YEp352. The cells at 85 and 87 were exposed to FK506, while those at 84 and 86 were not.

Data in Figure 8A demonstrate that, in the absence of FK506, FKBP and CNA2 showed no detectable interaction (84). In the presence of FK506, however, the proteins interacted (85), presumably because FK506 formed a complex with FKBP, which then bound CNA2 (Cyert).

Data in Figure 8A further show that, in the absence of FK506, CNI had no effect on the lack of interaction between FKBP and CNA2 (86). In the presence of FK506 (87), however, CNI potentiated, or enhanced the binding between FKBP and CNA2 (compare the intensity at 87 with that at 85). This effect suggests that CNI and similar compounds may be employed to increase the sensitivity of calcineurin to immunosuppressant drugs that act on it, and in this way, decrease the amount of the immunosuppressant required for a particular level of immunosuppression.

Experiments illustrated in Figures 9A and 9B demonstrate that CNI overproduction had little or no effect on the binding of CNA2 to CNB1, providing support for the specificity of the stimulatory effect that CNI overproduction had on the FK506-dependent binding of FKBP to calcineurin. The legends for Fig. 9A and 9B are shown in Figures 9B and 9D, respectively.

- 5 Locations of yeast colonies expressing the following constructs: 88:GBT-A2, GAD-B1 and YEp352, 89:GBT-A2, GAD-B1 and YEp352, 90:GBT-A2, GAD-B1 and CNI/YEp352, and 91:GBT-A2, GAD-B1 and CNI/YEp352. The colonies at 89 and 91 were exposed to FK506, while colonies at 88 and 90 were not.

- 10 Taken together, the above data show that overexpression of the full-length CNI clone markedly enhanced the FK506-dependent interaction of FKBP with CNA, although it didn't affect the interaction between CNA and CNB1.

EXAMPLE 5

Co-Immunoprecipitation of CN1c and CNA

- 15 Yeast BJ2407 harboring AS-CN1c, which carries an influenza hemagglutinin (HA) epitope tag (Wilson, *et al.*), and GAD-A2 (lanes 1, 3) or A2/YEp352 (lanes 2, 5), and strain MCY300-1 (*cna1⁻cna2⁻*; lane 4) were grown in selective media to OD₆₀₀=0.8. The cells were harvested, lysed, and immunoprecipitated in the presence of 25 µg/ml FK506 with anti-HA monoclonal antibody (obtained from M. Kirschner, Harvard University, Boston, MA; Wilson, *et al.*), following protocols described in Harlow, *et al.* The cell extracts (lanes 3-5) and the immune complex (lanes 1, 2) were resolved by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Laemmli) followed by western blot with a rabbit anti-CNA2 polyclonal antibody generated using standard methods (Harlow, *et al.*). Bound anti-CNA2 antibody was visualized with the "ECL" kit (Amersham, Arlington Heights, IL) using goat anti-
20 rabbit antibody. Molecular weight markers are indicated on the right in kD.

The results demonstrate that CN1c was capable of binding to CNA2 tightly enough for the complex to be co-immunoprecipitated. This independent, biochemical assay confirmed the results described above obtained using the two hybrid protein interaction assay — that is, that CN1c physically interacted with and bound CNA subunits.

- 30 Cell extracts of BJ2407 harboring AS-CN1c, and GAD-A2 or A1/Yep351, and Y153b1 harboring AS-CN1c and GAD-A1 were subjected to SDS-PAGE followed by western blot with anti HA antibody. The results showed that CN1c was present at very low levels *in vivo*.

The results are consistent with the observations that a limited amount of CNA2 was precipitated by anti-HA antibody recognizing the CN1c fusions, and that CN1 contains PEST-like motifs, a feature of proteins with a short half-life *in vivo* (Rogers, *et al.*).

5

EXAMPLE 6

Northern Blot of CN1c

Norther blots (*e.g.*, Sambrook, *et al.*) of yeast total RNA were hybridized with a CN1c probe. Exemplary data are shown in Figure 11. 20 μ g yeast RNA from YPH499 (lane 1) and MCY300-1 (lane 2) was resolved in a formaldehyde-agarose gel, transferred onto "HYBOND N+" membrane (Amersham, Arlington Heights, IL), and hybridized with 5×10^6 cpm/ml probe of the CN1c insert (1.22kb). A single message of approximately 2.9 kb was detected in both strains at about the same level following an 18-hour exposure on XAR5 film (Eastman Kodak, Rochester, NY).

The data indicate that CN1 was a physiologically expressed gene encoding a 2.9 kb message in yeast.

15

EXAMPLE 7

Chromosome Mapping of CN1c

A yeast chromosome blot obtained from the ATCC was hybridized with probe of the CN1c insert following the Southern hybridization procedure described in Sambrook, *et al.* A positive hybridization signal was obtained with two ATCC yeast genomic λ clones derived from chromosome 11. Clone 70500 had a relatively strong signal, while clone 70590 had a somewhat weaker one. A phage lysates of clone 70500 was ordered from the ATCC, amplified, purified, restriction-mapped, and used as a DNA source for cloning full length CN1 (Example 1).

25

EXAMPLE 8

CN1 null Mutants

1. Construction of *cni* Null Mutation

30

A 5', 1.8 kb *Bgl*III-*Hind*III and a 3', 0.9 kb *Xba*I-*Bgl*III fragment of CN1 were ligated into pRS305(LEU2) (Sikorski, *et al.*). The resultant plasmid had a deletion of a 2 kb *Hind*III-*Xba*I fragment from the coding sequence of CN1. This *cni::LEU2* mutant was introduced into the genomes of yeast haploid strains YPH499 (Sikorski, *et al.*), MCY300-1 (*cna1⁻ cna2⁻*) and DD12 (*cnb1⁻*) (Cyert, *et al.*, 1991, Cyert, *et al.*, 1992) as well as two diploid strains.

Leucine prototrophs were isolated at high frequency from all strains, and hybridization analysis confirmed that the *cni::LEU2* allele had replaced the CNI gene. The experiments indicate that CNI is not essential for viability, since CNI deletion mutant strains (even *cni⁻ cni⁻* double mutants) can survive.

5 *CNI* was deleted from three yeast strains: YPH499 (WT), MCY300-1 (*cna1⁻cna2⁻*), and DD12 (*cnb1⁻*), resulting in *cni⁻* strains LHy499, LHy300 and LHy12, respectively. Cells representing four colonies of each *cni* knockout strain and two colonies of each parent strain were grown in liquid YPD (Sherman, *et al.*) to saturation. Same numbers of cells from each culture were then plated onto YPD+Hygromycin B (40 μ g/ml) and growth was monitored at
10 30°C.

CNI deletions in each strain rendered that strain more resistant to hygromycin B. The effect was particularly pronounced in both MCY300-1 and DD12, suggesting that CNI functions as a suppressor of CN mutant's sensitivity to hygromycin B. The data indicate that deletion of *CNI* results in higher resistance to hygromycin B.

15

EXAMPLE 9

Isolation of CNI/ β -Galactosidase Fusion Protein

A CNI coding sequence is cloned into the λ -gt11 vector (Stratagene, La Jolla, CA). The coding frame is cloned in-frame to the β -galactosidase coding sequences present in λ gt11.
20 Bacterial lysogens infected either with lambda phage gt11 or with gt11/CNI are incubated in 32°C until the culture reaches to an O.D. of 0.4. Then the culture is incubated in a 43°C water bath for 15 minutes to induce gt11 peptide synthesis, and further incubated at 37°C for 1 hour. Bacterial cells are pelleted and lysed in lysis buffer (10 mM Tris, pH 7.4, 2 % "TRITON X-100" and 1% aprotinin). Bacterial lysates are clarified by centrifugation (10K,
25 for 10 minutes, Sorvall JA20 rotor) and the clarified lysates are incubated with Sepharose 4B beads conjugated with anti- β -galactosidase (Promega).

Binding and elution of β -galactosidase fusion proteins are performed according to the manufacturer's instruction. Typically binding of the proteins and washing of the column are done with lysis buffer. Bound proteins are eluted with 0.1 M carbonate/bicarbonate buffer,
30 pH 10.

While the invention has been described with reference to specific methods and embodiments, it will be appreciated that various modifications and changes may be made without departing from the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: The Board of Trustees of the Leland Stanford Junior University
- (ii) TITLE OF INVENTION: Calcineurin Interacting Protein Compositions and Methods
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dehlinger & Associates
 - (B) STREET: 350 Cambridge Avenue, Suite 250
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94306
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-OCT-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/328,322
 - (B) FILING DATE: 24-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sholtz, Charles K.
 - (B) REGISTRATION NUMBER: P38,615
 - (C) REFERENCE/DOCKET NUMBER: 8600-0151.41
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 324-0880
 - (B) TELEFAX: (415) 324-0960

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Sau3AI fragment containing CN1c coding sequence
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAT CAA AGT AGC AAT GTC TTC GCA TCC AAA CAG CTG GTC GCA AAC ATT Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln Leu Val Ala Asn Ile 1 5 10 15	48
TAT AAG CCC AAT CAG ATT CCA AGA GAA TTA ACT TCT CCT CAG GCG TTA Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr Ser Pro Gln Ala Leu 20 25 30	96
CCA TTA TCG CCC ATC ACC TCA CCA ATT CTC AAT TAC CAA CCA TTA TCA Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn Tyr Gln Pro Leu Ser 35 40 45	144
AAC TCC CCG CCT CCA GAT TTT GAT TTT GAT CTA GCT AAG CGC GGC GCA Asn Ser Pro Pro Pro Asp Phe Asp Phe Asp Leu Ala Lys Arg Gly Ala 50 55 60	192
GCC GAT TCT CAT GCT ATT CCT GTG GAT CCT CCA TCA TAT TTT GAT GTA Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro Ser Tyr Phe Asp Val 65 70 75 80	240
TTA AAG GCC GAT GGG ATT GAA TTG CCA TAC TAC GAT ACA AGT TCA TCT Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr Asp Thr Ser Ser Ser 85 90 95	288
AAA ATT CCT GAA CTA AAA CTA AAC AAA TCT AGA GAG ACA TTG GCC AGC Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg Glu Thr Leu Ala Ser 100 105 110	336
ATT GAG GAG GAC TCA TTC AAT GGT TGG TCT CAA ATT GAT GAC TTA TCC Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln Ile Asp Asp Leu Ser 115 120 125	384
GAC GAA GAT GAC AAT GAT GGC GAT ATA GCA TCT GGT TTC AAC TTC AAG Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser Gly Phe Asn Phe Lys 130 135 140	432
CTG TCA ACC AGT GCT CCG AGT GAG AAC GTT AAT TCA CAC ACT CCT ATT Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn Ser His Thr Pro Ile 145 150 155 160	480
TTG CAG TCT TTA AAC ATG AGT CTT GAT GGG AGA AAA AAA AAT CGT GCC Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg Lys Lys Asn Arg Ala 165 170 175	528
AGT CTA CAC GCA ACA TCA GTG TTA CCT AGT ACA ATA AGA CAG AAC AAT Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr Ile Arg Gln Asn Asn 180 185 190	576
CAG CAT TTC AAT GAC ATA AAC CAG ATG CTA GGC AGT AGT GAC GAA GAT Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly Ser Ser Asp Glu Asp 195 200 205	624
GCC TTT CCC AAA AGC CAA TCA TTA AAT TTC AAT AAG AAA CTA CCA ATA Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn Lys Lys Leu Pro Ile 210 215 220	672
CTT AAA ATT AAT GAT AAC GTC ATA CAA TCA AAC AGC AAT AGT AAT AAC Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn Ser Asn Ser Asn Asn 225 230 235 240	720
AGA GTT GAT AAT CCA GAA GAT ACA GTG GAT TCT TCA GTC GAT ATT ACA Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser Ser Val Asp Ile Thr 245 250 255	768

40

GCA TTT TAT GAT CCA AGA ATG TCA TCA GAT TCC AAA TTT GAT TGG GAG	816
Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser Lys Phe Asp Trp Glu	
260 265 270	
GTA AGC AAG AAC CAT GTT GAC CCA GCA GCC TAC TCG GTT AAC GTT GCT	864
Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr Ser Val Asn Val Ala	
275 280 285	
AGT GAA AAC CGT GTA CTG GAC GAC TTT AAG AAA GCA TTT CGC GAA AAG	912
Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys Ala Phe Arg Glu Lys	
290 295 300	
AGA AAA TAAGTACATT ATTTTCATTC TCCGACAGAA TTGCTACCAT TTTACTTTGT	968
Arg Lys	
305	
GTCCTGTGAT TCAATAGTGT ACAATATATT GGACATTTTA TAGTATACAA ATATACACCA	1028
TCAATCTATA CATCCATATC ACTTGTCGTA AAGATATCCC TTTTAAATAG TACAGCGATT	1088
AAAAAATAA CATGATTAAC GTTCAGTTAC CAATGAGCTT ATTTATTAGG CTTGCTTTAG	1148
ATTTTCCAA GTCAATTTTT GTTTTTTCTA ACGCTTGCAA CCTCATCTCA ACCTTCTTCC	1208
TTTGCAAGCA GATC	1222

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln Leu Val Ala Asn Ile	
1 5 10 15	
Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr Ser Pro Gln Ala Leu	
20 25 30	
Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn Tyr Gln Pro Leu Ser	
35 40 45	
Asn Ser Pro Pro Pro Asp Phe Asp Phe Asp Leu Ala Lys Arg Gly Ala	
50 55 60	
Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro Ser Tyr Phe Asp Val	
65 70 75 80	
Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr Asp Thr Ser Ser Ser	
85 90 95	
Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg Glu Thr Leu Ala Ser	
100 105 110	
Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln Ile Asp Asp Leu Ser	
115 120 125	
Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser Gly Phe Asn Phe Lys	
130 135 140	
Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn Ser His Thr Pro Ile	
145 150 155 160	

Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg Lys Lys Asn Arg Ala
 165 170 175
 Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr Ile Arg Gln Asn Asn
 180 185 190
 Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly Ser Ser Asp Glu Asp
 195 200 205
 Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn Lys Lys Leu Pro Ile
 210 215 220
 Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn Ser Asn Ser Asn Asn
 225 230 235 240
 Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser Ser Val Asp Ile Thr
 245 250 255
 Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser Lys Phe Asp Trp Glu
 260 265 270
 Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr Ser Val Asn Val Ala
 275 280 285
 Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys Ala Phe Arg Glu Lys
 290 295 300
 Arg Lys
 305

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CINC coding sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCAAAGTA GCAATGTCTT CGCATCCAAA CAGCTGGTCG CAAACATTTA TAAGCCCAAT	60
CAGATTCCAA GAGAATTAAC TTCTCCTCAG GCGTTACCAT TATCGCCCAT CACCTCACCA	120
ATTCTCAATT ACCAACCATT ATCAAACCTC CCGCCTCCAG ATTTTGATT TGTATCTAGCT	180
AAGCGCGGCG CAGCCGATTC TCATGCTATT CCTGTGGATC CTCCATCATA TTTTGATGTA	240
TTAAAGGCCG ATGGGATTGA ATTGCCATAC TACGATACAA GTTCATCTAA AATTCCTGAA	300
CTAAACTAA ACAAATCTAG AGAGACATTG GCCAGCATTG AGGAGGACTC ATTCAATGGT	360
TGGTCTCAAA TTGATGACTT ATCCGACGAA GATGACAATG ATGGCGATAT AGCATCTGGT	420
TTCAACTTCA AGCTGTCAAC CAGTGCTCCG AGTGAGAACG TTAATTCACA CACTCCTATT	480
TTGCAGTCTT TAAACATGAG TCTTGATGGG AGAAAAAAA ATCGTGCCAG TCTACACGCA	540

ACATCAGTGT TACCTAGTAC AATAAGACAG AACAATCAGC ATTTCAATGA CATAAACCAG 600
 ATGCTAGGCA GTAGTGACGA AGATGCCTTT CCCAAAAGCC AATCATTAAA TTTCAATAAG 660
 AAACTACCAA TACTTAAAT TAATGATAAC GTCATACAAT CAAACAGCAA TAGTAATAAC 720
 AGAGTTGATA ATCCAGAAGA TACAGTGGAT TCTTCAGTCG ATATTACAGC ATTTTATGAT 780
 CCAAGAATGT CATCAGATTC CAAATTTGAT TGGGAGGTAA GCAAGAACCA TGTTGACCCA 840
 GCAGCCTACT CGGTTAACGT TGCTAGTGAA AACCGTGAC TGGACGACTT TAAGAAAGCA 900
 TTTCGCGAAA AGAGAAAA 918

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full CNI coding sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 376..3120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGAACACTT CCTTCGAGAG AGTGCATTTT ACTATGTGAA CCAATTTTTC CTCTTTTTCG 60
 GTTTGCAAGT TCACCTGAAA AACTGCTTAA CACTACTAGC AATTGCCCTA TTGTCGTACG 120
 AGGACTTTGC CAAATGTATT CCCGGCTGTT TGTAGTATAT ATACGCAGAT ATATAATAGC 180
 GCCGTCTTTT TACCTCTTTG AGCGAATTGC CAAATATTGA CTCTTTTGTC TTATTTCGCT 240
 ATCCCCATCT TATCAAAAAT GGAACAACCT CGTTGAAATA AGAGACAAGC AACAAGAAAG 300
 ACAACCAACA GAAAGTTCCA TTCCGCACAA ATACGCTGGA ATCCCATAGA ATATTGCTTG 360
 TTCCTCTATG ACTAC ATG CTC CAA TTC AAT ACA GAA AAT GAT ACT GTA GCT 411
 Met Leu Gln Phe Asn Thr Glu Asn Asp Thr Val Ala
 1 5 10

CCA GTG TTT CCC ATG GAG CAA GAT ATA AAT GCA GCA CCT GAT GCC GTC 459
 Pro Val Phe Pro Met Glu Gln Asp Ile Asn Ala Ala Pro Asp Ala Val
 15 20 25

CCA CTG GTG CAG ACA ACA ACA CTA CAA GTC TTT GTA AAG CTT GCC GAA 507
 Pro Leu Val Gln Thr Thr Thr Leu Gln Val Phe Val Lys Leu Ala Glu
 30 35 40

CCC ATA GTG TTT TTA AAA GGA TTT GAA ACT AAC GGA CTG TCT GAA ATA 555
 Pro Ile Val Phe Leu Lys Gly Phe Glu Thr Asn Gly Leu Ser Glu Ile
 45 50 55 60

GCC CCC AGT ATC TTA CGA GGA TCT CTT ATC GTC AGG GTG TTG AAA CCG Ala Pro Ser Ile Leu Arg Gly Ser Leu Ile Val Arg Val Leu Lys Pro 65 70 75	603
AAT AAA TTA AAA AGT ATA TCG ATA ACC TTC AAA GGA ATA TCC AGA ACA Asn Lys Leu Lys Ser Ile Ser Ile Thr Phe Lys Gly Ile Ser Arg Thr 80 85 90	651
GAG TGG CCG GAA GGT ATA CCA CCG AAG AGA GAA GAA TTT TCA GAT GTT Glu Trp Pro Glu Gly Ile Pro Pro Lys Arg Glu Glu Phe Ser Asp Val 95 100 105	699
GAA ACT GTT GTC AAT CAC ACA TGG CCA TTT TAT CAG GCG GAT GAC GGC Glu Thr Val Val Asn His Thr Trp Pro Phe Tyr Gln Ala Asp Asp Gly 110 115 120	747
ATG AAT TCT TTC ACC TTA GAA CAT CAC AGC TCA AAT AAT TCG TCC AAT Met Asn Ser Phe Thr Leu Glu His His Ser Ser Asn Asn Ser Ser Asn 125 130 135 140	795
CGC CCA TCT ATG AGC GAT GAA GAT TAT CTA CTT GAA AAA AGC GGT GCT Arg Pro Ser Met Ser Asp Glu Asp Tyr Leu Leu Glu Lys Ser Gly Ala 145 150 155	843
TCA GTA TAT ATC CCA CCA ACC GCT GAA CCC CCT AAA GAT AAT AGC AAT Ser Val Tyr Ile Pro Pro Thr Ala Glu Pro Pro Lys Asp Asn Ser Asn 160 165 170	891
CTA AGT CTG GAT GCC TAT GAG CGC AAC TCA TTG TCA TCC GAT AAT TTG Leu Ser Leu Asp Ala Tyr Glu Arg Asn Ser Leu Ser Ser Asp Asn Leu 175 180 185	939
AGT AAC AAG CCA GTA TCA AGT GAT GTT TCC CAT GAC GAC AGT AAA CTG Ser Asn Lys Pro Val Ser Ser Asp Val Ser His Asp Asp Ser Lys Leu 190 195 200	987
TTG GCT ATT CAA AAG ACA CCA TTA CCA TCA TCT AGT CGA AGA GGA TCG Leu Ala Ile Gln Lys Thr Pro Leu Pro Ser Ser Ser Arg Arg Gly Ser 205 210 215 220	1035
GTA CCG GCA AAT TTT CAC GGT AAC TCT TTG TCA CCT CAT ACC TTC ATA Val Pro Ala Asn Phe His Gly Asn Ser Leu Ser Pro His Thr Phe Ile 225 230 235	1083
TCT GAT TTG TTC ACA AAA ACA TTC AGT AAT AGT GGC GCT ACT CCA AGT Ser Asp Leu Phe Thr Lys Thr Phe Ser Asn Ser Gly Ala Thr Pro Ser 240 245 250	1131
CCT GAG CAA GAG GAT AAC TAT CTT ACA CCA TCC AAA GAT TCT AAA GAA Pro Glu Gln Glu Asp Asn Tyr Leu Thr Pro Ser Lys Asp Ser Lys Glu 255 260 265	1179
GTT TTT ATT TTT CGA CCG GGC GAT TAT ATT TAC ACT TTT GAA CAG CCA Val Phe Ile Phe Arg Pro Gly Asp Tyr Ile Tyr Thr Phe Glu Gln Pro 270 275 280	1227
ATA TCG CAA TCT TAT CCA GAA AGT ATA AAA GCC AAT TTT GGT TCC GTG Ile Ser Gln Ser Tyr Pro Glu Ser Ile Lys Ala Asn Phe Gly Ser Val 285 290 295 300	1275
GAG TAT AAA CTG TCA ATA GAC ATA GAG AGG TTT GGC GCA TTC AAA TCA Glu Tyr Lys Leu Ser Ile Asp Ile Glu Arg Phe Gly Ala Phe Lys Ser 305 310 315	1323
ACT ATA CAT ACT CAA TTA CCC ATC AAA GTC GTA AGG CTT CCT TCT GAT Thr Ile His Thr Gln Leu Pro Ile Lys Val Val Arg Leu Pro Ser Asp 320 325 330	1371

GGA TCC GTA GAA GAG ACT GAA GCT ATT GCA ATT TCC AAG GAC TGG AAA Gly Ser Val Glu Glu Thr Glu Ala Ile Ala Ile Ser Lys Asp Trp Lys 335 340 345	1419
GAT CTT CTT CAT TAT GAC GTG GTA ATT TTC TCG AAA GAG ATC GTT TTG Asp Leu Leu His Tyr Asp Val Val Ile Phe Ser Lys Glu Ile Val Leu 350 355 360	1467
AAT GCA TTT TTA CCC ATC GAT TTC CAT TTC GCT CCT CTA GAT AAA GTT Asn Ala Phe Leu Pro Ile Asp Phe His Phe Ala Pro Leu Asp Lys Val 365 370 375 380	1515
ACT CTG CAT CGT ATT AGA ATT TAT CTA ACA GAG TCT ATG GAA TAC ACT Thr Leu His Arg Ile Arg Ile Tyr Leu Thr Glu Ser Met Glu Tyr Thr 385 390 395	1563
TGT AAT AGT AAT GGA AAT CAC GAG AAG GCT CGT AGA TTA GAG CCA ACT Cys Asn Ser Asn Gly Asn His Glu Lys Ala Arg Arg Leu Glu Pro Thr 400 405 410	1611
AAA AAG TTT CTG TTG GCT GAA CAT AAC GGT CCT AAA CTG CCT CAT ATA Lys Lys Phe Leu Leu Ala Glu His Asn Gly Pro Lys Leu Pro His Ile 415 420 425	1659
CCA GCT GGT TCG AAT CCT TTG AAG GCT AAA AAT AGA GGG AAC ATC CTC Pro Ala Gly Ser Asn Pro Leu Lys Ala Lys Asn Arg Gly Asn Ile Leu 430 435 440	1707
TTG GAT GAA AAA TCC GGC GAT CTA GTT AAC AAA GAT TTT CAG TTC GAG Leu Asp Glu Lys Ser Gly Asp Leu Val Asn Lys Asp Phe Gln Phe Glu 445 450 455 460	1755
GTG TTT GTC CCA AGC AAG TTT ACA AAC AGT ATA CGG TTA CAC CCT GAT Val Phe Val Pro Ser Lys Phe Thr Asn Ser Ile Arg Leu His Pro Asp 465 470 475	1803
ACA AAT TAT GAT AAA ATC AAA GCC CAC CAT TGG ATA AAA ATT TGC CTT Thr Asn Tyr Asp Lys Ile Lys Ala His His Trp Ile Lys Ile Cys Leu 480 485 490	1851
CGT CTT TCC AAG AAG TAC GGG GAC AAT AGA AAA CAT TTC GAA ATA AGT Arg Leu Ser Lys Lys Tyr Gly Asp Asn Arg Lys His Phe Glu Ile Ser 495 500 505	1899
ATT GAT TCT CCA ATC CAT ATT TTA AAT CAA CTA TGC TCA CAC GCG AAT Ile Asp Ser Pro Ile His Ile Leu Asn Gln Leu Cys Ser His Ala Asn 510 515 520	1947
ACT TTG CTA CCG AGC TAC GAG AGT CAT TTC CAG TAT TGT GAT GAA GAT Thr Leu Leu Pro Ser Tyr Glu Ser His Phe Gln Tyr Cys Asp Glu Asp 525 530 535 540	1995
GGT AAT TTC GCA CCA GCA GCA GAT CAA CAA AAT TAC GCA AGT CAT CAT Gly Asn Phe Ala Pro Ala Ala Asp Gln Gln Asn Tyr Ala Ser His His 545 550 555	2043
GAT TCC AAT ATT TTC TTC CCA AAA GAA GTT CTT TCG TCT CCC GTT CTT Asp Ser Asn Ile Phe Phe Pro Lys Glu Val Leu Ser Ser Pro Val Leu 560 565 570	2091
TCA CCT AAC GTG CAG AAG ATG AAC ATT AGA ATA CCG TCT GAT CTT CCA Ser Pro Asn Val Gln Lys Met Asn Ile Arg Ile Pro Ser Asp Leu Pro 575 580 585	2139
GTA GTG CGT AAT AGA GCT GAA AGC GTA AAG AAA AGC AAG TCA GAT AAT Val Val Arg Asn Arg Ala Glu Ser Val Lys Lys Ser Lys Ser Asp Asn 590 595 600	2187

ACC TCC AAG AAG AAT GAT CAA AGT AGC AAT GTC TTC GCA TCC AAA CAG Thr Ser Lys Lys Asn Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln 605 610 615 620	2235
CTG GTC GCA AAC ATT TAT AAG CCC AAT CAG ATT CCA AGA GAA TTA ACT Leu Val Ala Asn Ile Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr 625 630 635	2283
TCT CCT CAG GCG TTA CCA TTA TCG CCC ATC ACC TCA CCA ATT CTC AAT Ser Pro Gln Ala Leu Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn 640 645 650	2331
TAC CAA CCA TTA TCA AAC TCC CCG CCT CCA GAT TTT GAT TTT GAT CTA Tyr Gln Pro Leu Ser Asn Ser Pro Pro Asp Phe Asp Phe Asp Leu 655 660 665	2379
GCT AAG CGC GGC GCA GCC GAT TCT CAT GCT ATT CCT GTG GAT CCT CCA Ala Lys Arg Gly Ala Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro 670 675 680	2427
TCA TAT TTT GAT GTA TTA AAG GCC GAT GGG ATT GAA TTG CCA TAC TAC Ser Tyr Phe Asp Val Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr 685 690 695 700	2475
GAT ACA AGT TCA TCT AAA ATT CCT GAA CTA AAA CTA AAC AAA TCT AGA Asp Thr Ser Ser Ser Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg 705 710 715	2523
GAG ACA TTG GCC AGC ATT GAG GAG GAC TCA TTC AAT GGT TGG TCT CAA Glu Thr Leu Ala Ser Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln 720 725 730	2571
ATT GAT GAC TTA TCC GAC GAA GAT GAC AAT GAT GGC GAT ATA GCA TCT Ile Asp Asp Leu Ser Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser 735 740 745	2619
GGT TTC AAC TTC AAG CTG TCA ACC AGT GCT CCG AGT GAG AAC GTT AAT Gly Phe Asn Phe Lys Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn 750 755 760	2667
TCA CAC ACT CCT ATT TTG CAG TCT TTA AAC ATG AGT CTT GAT GGG AGA Ser His Thr Pro Ile Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg 765 770 775 780	2715
AAA AAA AAT CGT GCC AGT CTA CAC GCA ACA TCA GTG TTA CCT AGT ACA Lys Lys Asn Arg Ala Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr 785 790 795	2763
ATA AGA CAG AAC AAT CAG CAT TTC AAT GAC ATA AAC CAG ATG CTA GGC Ile Arg Gln Asn Asn Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly 800 805 810	2811
AGT AGT GAC GAA GAT GCC TTT CCC AAA AGC CAA TCA TTA AAT TTC AAT Ser Ser Asp Glu Asp Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn 815 820 825	2859
AAG AAA CTA CCA ATA CTT AAA ATT AAT GAT AAC GTC ATA CAA TCA AAC Lys Lys Leu Pro Ile Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn 830 835 840	2907
AGC AAT AGT AAT AAC AGA GTT GAT AAT CCA GAA GAT ACA GTG GAT TCT Ser Asn Ser Asn Asn Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser 845 850 855 860	2955

TCA GTC GAT ATT ACA GCA TTT TAT GAT CCA AGA ATG TCA TCA GAT TCC	3003
Ser Val Asp Ile Thr Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser	
865 870 875	
AAA TTT GAT TGG GAG GTA AGC AAG AAC CAT GTT GAC CCA GCA GCC TAC	3051
Lys Phe Asp Trp Glu Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr	
880 885 890	
TCG GTT AAC GTT GCT AGT GAA AAC CGT GTA CTG GAC GAC TTT AAG AAA	3099
Ser Val Asn Val Ala Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys	
895 900 905	
GCA TTT CGC GAA AAG AGA AAA TAAGTACATT ATTTTCATTC TCCGACAGAA	3150
Ala Phe Arg Glu Lys Arg Lys	
910 915	
TTGCTACCAT TTTACTTTGT GTCCTGTGAT TCAATAGTGT ACAATATATT GGACATTTTA	3210
TAGTATACAA ATATACACCA TCAATCTATA CATCCATATC ACTTGTCGTA AAGATATCCC	3270
TTTTTAATAG TACAGCGATT AAAAAATAA CATGATTAAC GTTCAGTTAC CAATGAGCTT	3330
ATTTATTAGG CTTGCTTTAG ATTTTCCAA GTCAATTTTT GTTTTTTCTA ACGCTTGCAA	3390
CCTCATCTCA ACCTTCTTCC TTTGCAAGCA GATCTTCGAA ACCATCTCGT TTATTCTCTC	3450
AATGCTGTTC CCACTTTCAT CATCGTCTGG GAAAAGTACC GGTAAGGGCG	3500

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Gln	Phe	Asn	Thr	Glu	Asn	Asp	Thr	Val	Ala	Pro	Val	Phe	Pro
1				5					10					15	
Met	Glu	Gln	Asp	Ile	Asn	Ala	Ala	Pro	Asp	Ala	Val	Pro	Leu	Val	Gln
			20					25					30		
Thr	Thr	Thr	Leu	Gln	Val	Phe	Val	Lys	Leu	Ala	Glu	Pro	Ile	Val	Phe
			35					40				45			
Leu	Lys	Gly	Phe	Glu	Thr	Asn	Gly	Leu	Ser	Glu	Ile	Ala	Pro	Ser	Ile
	50					55					60				
Leu	Arg	Gly	Ser	Leu	Ile	Val	Arg	Val	Leu	Lys	Pro	Asn	Lys	Leu	Lys
65					70					75				80	
Ser	Ile	Ser	Ile	Thr	Phe	Lys	Gly	Ile	Ser	Arg	Thr	Glu	Trp	Pro	Glu
				85					90					95	
Gly	Ile	Pro	Pro	Lys	Arg	Glu	Glu	Phe	Ser	Asp	Val	Glu	Thr	Val	Val
			100					105					110		
Asn	His	Thr	Trp	Pro	Phe	Tyr	Gln	Ala	Asp	Asp	Gly	Met	Asn	Ser	Phe
			115				120					125			
Thr	Leu	Glu	His	His	Ser	Ser	Asn	Asn	Ser	Ser	Asn	Arg	Pro	Ser	Met
	130					135						140			

Ser Asp Glu Asp Tyr Leu Leu Glu Lys Ser Gly Ala Ser Val Tyr Ile
 145 150 155 160
 Pro Pro Thr Ala Glu Pro Pro Lys Asp Asn Ser Asn Leu Ser Leu Asp
 165 170 175
 Ala Tyr Glu Arg Asn Ser Leu Ser Ser Asp Asn Leu Ser Asn Lys Pro
 180 185 190
 Val Ser Ser Asp Val Ser His Asp Asp Ser Lys Leu Leu Ala Ile Gln
 195 200 205
 Lys Thr Pro Leu Pro Ser Ser Ser Arg Arg Gly Ser Val Pro Ala Asn
 210 215 220
 Phe His Gly Asn Ser Leu Ser Pro His Thr Phe Ile Ser Asp Leu Phe
 225 230 235 240
 Thr Lys Thr Phe Ser Asn Ser Gly Ala Thr Pro Ser Pro Glu Gln Glu
 245 250 255
 Asp Asn Tyr Leu Thr Pro Ser Lys Asp Ser Lys Glu Val Phe Ile Phe
 260 265 270
 Arg Pro Gly Asp Tyr Ile Tyr Thr Phe Glu Gln Pro Ile Ser Gln Ser
 275 280 285
 Tyr Pro Glu Ser Ile Lys Ala Asn Phe Gly Ser Val Glu Tyr Lys Leu
 290 295 300
 Ser Ile Asp Ile Glu Arg Phe Gly Ala Phe Lys Ser Thr Ile His Thr
 305 310 315 320
 Gln Leu Pro Ile Lys Val Val Arg Leu Pro Ser Asp Gly Ser Val Glu
 325 330 335
 Glu Thr Glu Ala Ile Ala Ile Ser Lys Asp Trp Lys Asp Leu Leu His
 340 345 350
 Tyr Asp Val Val Ile Phe Ser Lys Glu Ile Val Leu Asn Ala Phe Leu
 355 360 365
 Pro Ile Asp Phe His Phe Ala Pro Leu Asp Lys Val Thr Leu His Arg
 370 375 380
 Ile Arg Ile Tyr Leu Thr Glu Ser Met Glu Tyr Thr Cys Asn Ser Asn
 385 390 395 400
 Gly Asn His Glu Lys Ala Arg Arg Leu Glu Pro Thr Lys Lys Phe Leu
 405 410 415
 Leu Ala Glu His Asn Gly Pro Lys Leu Pro His Ile Pro Ala Gly Ser
 420 425 430
 Asn Pro Leu Lys Ala Lys Asn Arg Gly Asn Ile Leu Leu Asp Glu Lys
 435 440 445
 Ser Gly Asp Leu Val Asn Lys Asp Phe Gln Phe Glu Val Phe Val Pro
 450 455 460
 Ser Lys Phe Thr Asn Ser Ile Arg Leu His Pro Asp Thr Asn Tyr Asp
 465 470 475 480
 Lys Ile Lys Ala His His Trp Ile Lys Ile Cys Leu Arg Leu Ser Lys
 485 490 495

Lys Tyr Gly Asp Asn Arg Lys His Phe Glu Ile Ser Ile Asp Ser Pro
 500 505 510
 Ile His Ile Leu Asn Gln Leu Cys Ser His Ala Asn Thr Leu Leu Pro
 515 520 525
 Ser Tyr Glu Ser His Phe Gln Tyr Cys Asp Glu Asp Gly Asn Phe Ala
 530 535 540
 Pro Ala Ala Asp Gln Gln Asn Tyr Ala Ser His His Asp Ser Asn Ile
 545 550 555 560
 Phe Phe Pro Lys Glu Val Leu Ser Ser Pro Val Leu Ser Pro Asn Val
 565 570 575
 Gln Lys Met Asn Ile Arg Ile Pro Ser Asp Leu Pro Val Val Arg Asn
 580 585 590
 Arg Ala Glu Ser Val Lys Lys Ser Lys Ser Asp Asn Thr Ser Lys Lys
 595 600 605
 Asn Asp Gln Ser Ser Asn Val Phe Ala Ser Lys Gln Leu Val Ala Asn
 610 615 620
 Ile Tyr Lys Pro Asn Gln Ile Pro Arg Glu Leu Thr Ser Pro Gln Ala
 625 630 635 640
 Leu Pro Leu Ser Pro Ile Thr Ser Pro Ile Leu Asn Tyr Gln Pro Leu
 645 650 655
 Ser Asn Ser Pro Pro Pro Asp Phe Asp Phe Asp Leu Ala Lys Arg Gly
 660 665 670
 Ala Ala Asp Ser His Ala Ile Pro Val Asp Pro Pro Ser Tyr Phe Asp
 675 680 685
 Val Leu Lys Ala Asp Gly Ile Glu Leu Pro Tyr Tyr Asp Thr Ser Ser
 690 695 700
 Ser Lys Ile Pro Glu Leu Lys Leu Asn Lys Ser Arg Glu Thr Leu Ala
 705 710 715 720
 Ser Ile Glu Glu Asp Ser Phe Asn Gly Trp Ser Gln Ile Asp Asp Leu
 725 730 735
 Ser Asp Glu Asp Asp Asn Asp Gly Asp Ile Ala Ser Gly Phe Asn Phe
 740 745 750
 Lys Leu Ser Thr Ser Ala Pro Ser Glu Asn Val Asn Ser His Thr Pro
 755 760 765
 Ile Leu Gln Ser Leu Asn Met Ser Leu Asp Gly Arg Lys Lys Asn Arg
 770 775 780
 Ala Ser Leu His Ala Thr Ser Val Leu Pro Ser Thr Ile Arg Gln Asn
 785 790 795 800
 Asn Gln His Phe Asn Asp Ile Asn Gln Met Leu Gly Ser Ser Asp Glu
 805 810 815
 Asp Ala Phe Pro Lys Ser Gln Ser Leu Asn Phe Asn Lys Lys Leu Pro
 820 825 830
 Ile Leu Lys Ile Asn Asp Asn Val Ile Gln Ser Asn Ser Asn Ser Asn
 835 840 845

Asn Arg Val Asp Asn Pro Glu Asp Thr Val Asp Ser Ser Val Asp Ile
 850 855 860
 Thr Ala Phe Tyr Asp Pro Arg Met Ser Ser Asp Ser Lys Phe Asp Trp
 865 870 875 880
 Glu Val Ser Lys Asn His Val Asp Pro Ala Ala Tyr Ser Val Asn Val
 885 890 895
 Ala Ser Glu Asn Arg Val Leu Asp Asp Phe Lys Lys Ala Phe Arg Glu
 900 905 910
 Lys Arg Lys
 915

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: coding sequence of CNI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCTCCAAT TCAATACAGA AAATGATACT GTAGCTCCAG TGTTCCTCAT GGAGCAAGAT	60
ATAAATGCAG CACCTGATGC CGTCCCCTG GTGCAGACAA CAACACTACA AGTCTTTGTA	120
AAGCTTGCCG AACCCATAGT GTTTTTAAAA GGATTGAAA CTAACGGACT GTCTGAAATA	180
CCCCCAGTA TCTTACGAGG ATCTCTTATC GTCAGGGTGT TGAACCGAA TAAATTAAAA	240
AGTATATCGA TAACCTTCAA AGGAATATCC AGAACAGAGT GGCCGGAAGG TATACCACCG	300
AAGAGAGAAG AATTTTCAGA TGTGAAACT GTTGCAATC ACACATGGCC ATTTTATCAG	360
GCGGATGACG GCATGAATTC TTTCACCTTA GAACATCACA GCTCAAATAA TTCGTCCAAT	420
CGCCCATCTA TGAGCGATGA AGATTATCTA CTTGAAAAA GCGGTGCTTC AGTATATATC	480
CCACCAACCG CTGAACCCCC TAAAGATAAT AGCAATCTAA GTCTGGATGC CTATGAGCGC	540
AACTCATTGT CATCCGATAA TTTGAGTAAC AAGCCAGTAT CAAGTGATGT TTCCCATGAC	600
GACAGTAAAC TGTGGCTAT TCAAAGACA CCATTACCAT CATCTAGTCG AAGAGGATCG	660
GTACCGGCAA ATTTTCACGG TAACTCTTTG TCACCTCATA CCTTCATATC TGATTTGTTC	720
ACAAAAACAT TCAGTAATAG TGGCGCTACT CCAAGTCCTG AGCAAGAGGA TAACTATCTT	780
ACACCATCCA AAGATTCTAA AGAAGTTTTT ATTTTTCGAC CGGGCGATTA TATTTACACT	840
TTTGAACAGC CAATATCGCA ATCTTATCCA GAAAGTATAA AAGCCAATTT TGGTTCOGTG	900
GAGTATAAAC TGTCAATAGA CATAGAGAGG TTTGGCGCAT TCAAATCAAC TATACATACT	960

CAATTACCCA TCAAAGTCGT AAGGCTTCCT TCTGATGGAT CCGTAGAAGA GACTGAAGCT	1020
ATTGCAATTT CCAAGGACTG GAAAGATCTT CTTCAATTATG ACGTGGTAAT TTTCTCGAAA	1080
GAGATCGTTT TGAATGCATT TTTACCCATC GATTTCATT TCGCTCCTCT AGATAAAGTT	1140
ACTCTGCATC GTATTAGAAT TTATCTAACA GAGTCTATGG AATACACTTG TAATAGTAAT	1200
GGAAATCACG AGAAGGCTCG TAGATTAGAG CCAACTAAAA AGTTTCTGTT GGCTGAACAT	1260
AACGGTCCTA AACTGCCTCA TATACCAGCT GGTTCGAATC CTTTGAAGGC TAAAAATAGA	1320
GGGAACATCC TCTTGATGA AAAATCCGGC GATCTAGTTA ACAAAGATTT TCAGTTCGAG	1380
GTGTTTGTCC CAAGCAAGTT TACAAACAGT ATACGGTTAC ACCCTGATAC AAATTATGAT	1440
AAAATCAAAG CCCACCATTG GATAAAAATT TGCCTTCGTC TTTCCAAGAA GTACGGGGAC	1500
AATAGAAAAC ATTTCGAAAT AAGTATTGAT TCTCCAATCC ATATTTTAAA TCAACTATGC	1560
TCACACGCGA ATACTTTGCT ACCGAGCTAC GAGAGTCATT TCCAGTATTG TGATGAAGAT	1620
GGTAATTTCC CACCAGCAGC AGATCAACAA AATTACGCAA GTCATCATGA TTCCAATATT	1680
TTCTTCCCAA AAGAAGTTCT TTCGTCTCCC GTTCTTTCAC CTAACGTGCA GAAGATGAAC	1740
ATTAGAATAC CGTCTGATCT TCCAGTAGTG CGTAATAGAG CTGAAAGCGT AAAGAAAAGC	1800
AAGTCAGATA ATACCTCCAA GAAGAATGAT CAAAGTAGCA ATGTCTTCGC ATCCAAACAG	1860
CTGGTCGCAA ACATTTATAA GCCCAATCAG ATTCCAAGAG AATTAAC TTCCTCAGGCG	1920
TTACCATTAT CGCCCATCAC CTCACCAATT CTCAATTACC AACCATTATC AACTCCCCG	1980
CCTCCAGATT TTGATTTTGA TCTAGCTAAG CGCGGCGCAG CCGATTCTCA TGCTATTCCT	2040
GTGGATCCTC CATCATATTT TGATGTATTA AAGGCCGATG GGATTGAATT GCCATACTAC	2100
GATACAAGTT CATCTAAAAT TCCTGAACTA AACTAAACA AATCTAGAGA GACATTGGCC	2160
AGCATTGAGG AGGACTCATT CAATGGTTGG TCTCAAATTG ATGACTTATC CGACGAAGAT	2220
GACAATGATG GCGATATAGC ATCTGGTTTC AACTTCAAGC TGTCAACCAG TGCTCCGAGT	2280
GAGAACGTTA ATTCACACAC TCCTATTTTG CAGTCTTTAA ACATGAGTCT TGATGGGAGA	2340
AAAAAAAATC GTGCCAGTCT ACACGCAACA TCAGTGTTAC CTAGTACAAT AAGACAGAAC	2400
AATCAGCATT TCAATGACAT AAACCAGATG CTAGGCAGTA GTGACGAAGA TGCCTTTCCC	2460
AAAAGCCAAT CATTAAATTT CAATAAGAAA CTACCAATAC TTAATAATTAA TGATAACGTC	2520
ATACAATCAA ACAGCAATAG TAATAACAGA GTTGATAATC CAGAAGATAC AGTGGATTCT	2580
TCAGTCGATA TTACAGCATT TTATGATCCA AGAATGTCAT CAGATTCCAA ATTTGATTGG	2640
GAGGTAAGCA AGAACCATGT TGACCCAGCA GCCTACTCGG TTAACGTTGC TAGTGAAAAC	2700
CGTGTAAGG ACGACTTTAA GAAAGCATTT CCGGAAAAGA GAAAA	2745

(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

51

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CNI-PRC-A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCAAAAAAG AGATCTCGGA TCAAAGTAGC

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: CNI-PCR-B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGTTTTTCA GTGTCGACGA TTCATAGATC

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1964 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full
CNA1 coding sequence

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 286..1944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTTGTTGCA TTTTGATATT CATCTATATC TATTTCAAAA TTTTTCATGT CATCGCCTCT

60

TGAAACATGA ATTTTCCAAT TCTGAAAAAG AACGTACTAC TGGGAAACAA AAGGGAAAAA	120
TGTATAAATC CTTTAATGTT TTTGAATCAA GAGGCATTAT TATAAAAGAA CGAAGCAAAG	180
CCTTTAATAT TTGCTTTATT AAAGGTATTA TTCAAAGAAA AGTTTTTTTA GATTCTTTTT	240
TTTTTGACGT ATTAGCTCAG CTGCCATAAA ACACTCTCAA CGCCA ATG TCG AAA	294
Met Ser Lys	
1	
GAC TTG AAT TCT TCA CGC ATC AAA ATC ATT AAA CCT AAT GAC TCT TAC	342
Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn Asp Ser Tyr	
5 10 15	
ATA AAG GTT GAC CGG AAA AAA GAT TTA ACA AAA TAC GAA TTA GAA AAC	390
Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu Leu Glu Asn	
20 25 30 35	
GGT AAA GTA ATT TCT ACT AAG GAC CGA TCC TAC GCT TCT GTA CCT GCC	438
Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser Val Pro Ala	
40 45 50	
ATA ACA GGA AAG ATA CCA AGT GAT GAG GAA GTA TTC GAC TCC AAG ACG	486
Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp Ser Lys Thr	
55 60 65	
GGA TTA CCT AAT CAT TCC TTT TTA AGA GAG CAT TTC TTT CAT GAG GGT	534
Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe His Glu Gly	
70 75 80	
CGA CTT TCT AAG GAA CAG GCC ATA AAA ATC TTA AAT ATG TCA ACT GTA	582
Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met Ser Thr Val	
85 90 95	
GCA TTG AGT AAA GAA CCC AAT CTA CTA AAA CTC AAA GCG CCA ATT ACT	630
Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala Pro Ile Thr	
100 105 110 115	
ATA TGT GGT GAT ATT CAC GGG CAG TAT TAT GAT TTA TTG AAA CTG TTT	678
Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu Lys Leu Phe	
120 125 130	
GAA GTT GGC GGT GAC CCC GCC GAA ATC GAC TAT TTA TTC TTG GGG GAT	726
Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe Leu Gly Asp	
135 140 145	
TAT GTT GAT AGA GGT GCA TTC TCT TTT GAG TGT CTG ATT TAT TTG TAC	774
Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr	
150 155 160	
TCC TTG AAG TTG AAT AAT TTA GGG AGA TTT TGG ATG CTA AGA GGT AAC	822
Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu Arg Gly Asn	
165 170 175	
CAT GAG TGT AAG CAC TTG ACC TCT TAT TTT ACT TTT AAG AAT GAG ATG	870
His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met	
180 185 190 195	
TTG CAC AAA TAC GAT ATG GAA GTT TAC GAT GCT TGC TGC AGA TCA TTC	918
Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys Arg Ser Phe	
200 205 210	
AAT GTC TTA CCA TTA GCA GCT TTA ATG AAC GGA CAA TAT TTT TGT GTG	966
Asn Val Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr Phe Cys Val	
215 220 225	

CAT GGT GGT ATC TCT CCA GAG TTA AAA TCA GTA GAG GAT GTT AAT AAA His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp Val Asn Lys 230 235 240	1014
ATT AAT AGA TTT CGA GAA ATC CCA TCT CGT GGT CTC ATG TGT GAC CTA Ile Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met Cys Asp Leu 245 250 255	1062
CTA TGG GCC GAT CCT GTC GAA AAT TAT GAT GAT GCA AGA GAT GGT AGC Leu Trp Ala Asp Pro Val Glu Asn Tyr Asp Asp Ala Arg Asp Gly Ser 260 265 270 275	1110
GAA TTT GAT CAG AGC GAG GAT GAA TTC GTA CCT AAC AGT TTG AGG GGT Glu Phe Asp Gln Ser Glu Asp Glu Phe Val Pro Asn Ser Leu Arg Gly 280 285 290	1158
TGC TCT TTC GCC TTC ACT TTT AAA GCA TCA TGC AAG TTT TTG AAG GCA Cys Ser Phe Ala Phe Thr Phe Lys Ala Ser Cys Lys Phe Leu Lys Ala 295 300 305	1206
AAT GGT TTG TTA TCT ATT ATT AGA GCA CAC GAA GCA CAG GAT GCT GCG Asn Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly 310 315 320	1254
TAC AGA ATG TAT AAA AAC AAT AAA GTA ACA GGC TTC CCG AGC TTA ATA Tyr Arg Met Tyr Lys Asn Asn Lys Val Thr Gly Phe Pro Ser Leu Ile 325 330 335	1302
ACC ATG TTC AGT GCG CCA AAC TAC CTG GAC ACA TAT CAT AAT AAA GCT Thr Met Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr His Asn Lys Ala 340 345 350 355	1350
GCT GTG TTA AAA TAT GAA GAA AAC GTC ATG AAC ATC AGG CAG TTT CAC Ala Val Leu Lys Tyr Glu Glu Asn Val Met Asn Ile Arg Gln Phe His 360 365 370	1398
ATG TCT CCG CAC CCT TAC TGG TTG CCT GAT TTT ATG GAT GTT TTC ACC Met Ser Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp Val Phe Thr 375 380 385	1446
TGG TCA CTA CCT TTT GTT GGC GAA AAA GTT ACT AGC ATG TTA GTG TCT Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Ser Met Leu Val Ser 390 395 400	1494
ATA TTA AAC ATA TGT AGT GAG CAG GAA CTT GAC CCA GAA TCG GAA CCC Ile Leu Asn Ile Cys Ser Glu Gln Glu Leu Asp Pro Glu Ser Glu Pro 405 410 415	1542
AAA GCT GCG GAG GAG ACT GTA AAG GCA AGA GCA AAC GCA ACT AAG GAG Lys Ala Ala Glu Glu Thr Val Lys Ala Arg Ala Asn Ala Thr Lys Glu 420 425 430 435	1590
ACC GGC ACC CCA TCT GAT GAA AAG GCG TCA TCA GCG ATA TTA GAA GAT Thr Gly Thr Pro Ser Asp Glu Lys Ala Ser Ser Ala Ile Leu Glu Asp 440 445 450	1638
GAA ACC CGA AGA AAG GCT TTG AGA AAT AAG ATA TTA GCT ATT GCT AAA Glu Thr Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala Ile Ala Lys 455 460 465	1686
GTT TCA AGA ATG TTT TCG GTG CTA AGA GAA GAG AGC GAA AAA GTG GAA Val Ser Arg Met Phe Ser Val Leu Arg Glu Glu Ser Glu Lys Val Glu 470 475 480	1734
TAT TTG AAA ACT ATG AAT GCC GGT GTC TTA CCT CGT GGT GCT CTA GCT Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly Ala Leu Ala 485 490 495	1782

54

CGT GGG ACT GAA GGT TTG AAT GAA ACG CTA AGC ACT TTT GAA AAG GCT	1830
Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu Ser Thr Phe Glu Lys Ala	
500 505 510 515	
AGA AAG GAA GAC CTT ATT AAT GAA AAA TTA CCA CCA TCT TTA TCG GAG	1878
Arg Lys Glu Asp Leu Ile Asn Glu Lys Leu Pro Pro Ser Leu Ser Glu	
520 525 530	
GTT GAA CAA GAG AAG ATT AAA TAC TAC GAA AAA ATA TTA AAG GGA GCG	1926
Val Glu Gln Glu Lys Ile Lys Tyr Tyr Glu Lys Ile Leu Lys Gly Ala	
535 540 545	
GAG AAA AAG CCA CAA CTG TGATAAATCT TCATTTTATT	1964
Glu Lys Lys Pro Gln Leu	
550	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Lys Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn	
1 5 10 15	
Asp Ser Tyr Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu	
20 25 30	
Leu Glu Asn Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser	
35 40 45	
Val Pro Ala Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp	
50 55 60	
Ser Lys Thr Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe	
65 70 75 80	
His Glu Gly Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met	
85 90 95	
Ser Thr Val Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala	
100 105 110	
Pro Ile Thr Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu	
115 120 125	
Lys Leu Phe Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe	
130 135 140	
Leu Gly Asp Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile	
145 150 155 160	
Tyr Leu Tyr Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu	
165 170 175	
Arg Gly Asn His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys	
180 185 190	
Asn Glu Met Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys	
195 200 205	

55

Arg Ser Phe Asn Val Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr
 210 215 220
 Phe Cys Val His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp
 225 230 235 240
 Val Asn Lys Ile Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met
 245 250 255
 Cys Asp Leu Leu Trp Ala Asp Pro Val Glu Asn Tyr Asp Asp Ala Arg
 260 265 270
 Asp Gly Ser Glu Phe Asp Gln Ser Glu Asp Glu Phe Val Pro Asn Ser
 275 280 285
 Leu Arg Gly Cys Ser Phe Ala Phe Thr Phe Lys Ala Ser Cys Lys Phe
 290 295 300
 Leu Lys Ala Asn Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln
 305 310 315 320
 Asp Ala Gly Tyr Arg Met Tyr Lys Asn Asn Lys Val Thr Gly Phe Pro
 325 330 335
 Ser Leu Ile Thr Met Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr His
 340 345 350
 Asn Lys Ala Ala Val Leu Lys Tyr Glu Glu Asn Val Met Asn Ile Arg
 355 360 365
 Gln Phe His Met Ser Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp
 370 375 380
 Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Ser Met
 385 390 395 400
 Leu Val Ser Ile Leu Asn Ile Cys Ser Glu Gln Glu Leu Asp Pro Glu
 405 410 415
 Ser Glu Pro Lys Ala Ala Glu Glu Thr Val Lys Ala Arg Ala Asn Ala
 420 425 430
 Thr Lys Glu Thr Gly Thr Pro Ser Asp Glu Lys Ala Ser Ser Ala Ile
 435 440 445
 Leu Glu Asp Glu Thr Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala
 450 455 460
 Ile Ala Lys Val Ser Arg Met Phe Ser Val Leu Arg Glu Glu Ser Glu
 465 470 475 480
 Lys Val Glu Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly
 485 490 495
 Ala Leu Ala Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu Ser Thr Phe
 500 505 510
 Glu Lys Ala Arg Lys Glu Asp Leu Ile Asn Glu Lys Leu Pro Pro Ser
 515 520 525
 Leu Ser Glu Val Glu Gln Glu Lys Ile Lys Tyr Tyr Glu Lys Ile Leu
 530 535 540
 Lys Gly Ala Glu Lys Lys Pro Gln Leu
 545 550

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full
 CNA2 coding sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 262..2073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAGTCTATA ATACGTTTGA TACAGCTAGA TATCGCTAGC GCCAACATTG TCCCCCTCTC	60
TTGATCAATG CTTTTTTTTCG GCCCGAGACA AATGAGAAAA TGTCCTAAAA ATACCTTTCA	120
TCAAGACTCC TATTTTTCCT TAGAAAAAAC ATATATCCAA CTGGAACAGT ATTAAGCCAA	180
TTGCTACGAT ACAAACAAAA GGAGATATTC CTTCCCTCCC ATAGAGTCAC ACAGGAGCCA	240
GTACTTCTTC TTGAACCCGC A ATG TCT TCA GAC GCT ATA AGA AAT ACT GAG	291
Met Ser Ser Asp Ala Ile Arg Asn Thr Glu	10
CAG ATA AAC GCC GCT ATT AAA ATT ATA GAA AAC AAA ACA GAG CGT CCG	339
Gln Ile Asn Ala Ala Ile Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro	25
CAA TCG TCC ACA ACC CCT ATA GAT TCG AAG GCT AGT ACA GTT GCT GCT	387
Gln Ser Ser Thr Thr Pro Ile Asp Ser Lys Ala Ser Thr Val Ala Ala	40
GCT AAT TCC ACG GCC ACA GAA ACT TCC AGA GAC CTT ACA CAA TAT ACC	435
Ala Asn Ser Thr Ala Thr Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr	55
CTA GAT GAC GGA AGA GTC GTA TCG ACA AAC CGC AGA ATA ATG AAT AAA	483
Leu Asp Asp Gly Arg Val Val Ser Thr Asn Arg Arg Ile Met Asn Lys	70
GTG CCC GCC ATC ACG TCA CAT GTT CCT ACA GAT GAA GAG CTG TTC CAG	531
Val Pro Ala Ile Thr Ser His Val Pro Thr Asp Glu Glu Leu Phe Gln	85
CCC AAT GGG ATA CCT CGT CAC GAA TTC CTA AGA GAT CAT TTC AAG CGC	579
Pro Asn Gly Ile Pro Arg His Glu Phe Leu Arg Asp His Phe Lys Arg	95
GAG GGC AAA TTG TCG GCT GCG CAG GCG GCC AGG ATC GTT ACA CTT GCA	627
Glu Gly Lys Leu Ser Ala Ala Gln Ala Ala Arg Ile Val Thr Leu Ala	110
ACG GAA CTC TTC AGC AAA GAA CCC AAC CTT ATA TCT GTT CCC GCC CCA	675
Thr Glu Leu Phe Ser Lys Glu Pro Asn Leu Ile Ser Val Pro Ala Pro	125

ATC ACA GTT TGC GGT GAT ATC CAT GGC CAG TAC TTT GAC CTT TTG AAG Ile Thr Val Cys Gly Asp Ile His Gly Gln Tyr Phe Asp Leu Leu Lys 140 145 150	723
CTA TTC GAA GTT GGC GGA GAT CCG GCC ACT ACA TCG TAT TTG TTC TTG Leu Phe Glu Val Gly Gly Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu 155 160 165 170	771
GGA GAC TAT GTC GAC AGA GGG TCC TTT TCG TTT GAG TGT CTT ATT TAT Gly Asp Tyr Val Asp Arg Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr 175 180 185	819
TTA TAT TCT TTG AAG CTG AAT TTT AAC GAC CAT TTC TGG CTA CTG AGG Leu Tyr Ser Leu Lys Leu Asn Phe Asn Asp His Phe Trp Leu Leu Arg 190 195 200	867
GGT AAC CAC GAA TGT AAG CAT CTA ACG TCA TAT TTC ACT TTC AAA AAT Gly Asn His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys Asn 205 210 215	915
GAA ATG CTG CAC AAG TAC AAT CTA GAT ATT TAC GAG AAA TGC TGC GAA Glu Met Leu His Lys Tyr Asn Leu Asp Ile Tyr Glu Lys Cys Cys Glu 220 225 230	963
TCG TTT AAC AAC TTG CCC CTG GCT GCG TTA ATG AAC GGA CAG TAT CTT Ser Phe Asn Asn Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr Leu 235 240 245 250	1011
TGT GTT CAT GGT GGT ATA TCT CCC GAG TTA AAC TCT TTA CAG GAC ATT Cys Val His Gly Gly Ile Ser Pro Glu Leu Asn Ser Leu Gln Asp Ile 255 260 265	1059
AAC AAC CTA AAT AGA TTC AGG GAG ATT CCC TCT CAT GGC CTG ATG TGT Asn Asn Leu Asn Arg Phe Arg Glu Ile Pro Ser His Gly Leu Met Cys 270 275 280	1107
GAT CTG TTG TGG GCT GAC CCG ATT GAA GAG TAC GAC GAA GTC TTG GAT Asp Leu Leu Trp Ala Asp Pro Ile Glu Glu Tyr Asp Glu Val Leu Asp 285 290 295	1155
AAA GAC TTG ACT GAG GAA GAC ATA GTG AAC TCC AAA ACC ATG GTT CCT Lys Asp Leu Thr Glu Glu Asp Ile Val Asn Ser Lys Thr Met Val Pro 300 305 310	1203
CAT CAT GGC AAG ATG GCA CCT TCA AGG GAT ATG TTT GTC CCA AAC TCA His His Gly Lys Met Ala Pro Ser Arg Asp Met Phe Val Pro Asn Ser 315 320 325 330	1251
GTA AGG GGC TGT TCA TAT GCC TTC ACG TAT CGT GCT GCG TGC CAT TTT Val Arg Gly Cys Ser Tyr Ala Phe Thr Tyr Arg Ala Ala Cys His Phe 335 340 345	1299
CTG CAA GAG ACT GGC CTG TTG TCC ATC ATC AGG GCA CAC GAG GCT CAA Leu Gln Glu Thr Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln 350 355 360	1347
GAC GCT GGT TAT AGA ATG TAC AAA AAT ACC AAG ACT TTG GGC TTT CCC Asp Ala Gly Tyr Arg Met Tyr Lys Asn Thr Lys Thr Leu Gly Phe Pro 365 370 375	1395
TCT CTT TTG ACC CTT TTC AGT GCG CCT AAC TAC TTG GAC ACC TAC AAT Ser Leu Leu Thr Leu Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr Asn 380 385 390	1443
AAT AAG GCT GCC ATA TTG AAA TAC GAA AAT AAT GTT ATG AAT ATC AGA Asn Lys Ala Ala Ile Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg 395 400 405 410	1491

58

CAA TTC AAC ATG ACT CCA CAC CCC TAT TGG TTA CCA GAT TTC ATG GAC Gln Phe Asn Met Thr Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp 415 420 425	1539
GTT TTC ACG TGG TCC TTG CCA TTT GTT GGT GAA AAA GTT ACA GAG ATG Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met 430 435 440	1587
CTT GTC GCA ATT CTA AAC ATC TGT ACT GAA GAT GAG CTG GAA AAC GAC Leu Val Ala Ile Leu Asn Ile Cys Thr Glu Asp Glu Leu Glu Asn Asp 445 450 455	1635
ACC CCC GTC ATT GAA GAA TTA GTT GGT ACC GAT AAA AAA TTG CCA CAA Thr Pro Val Ile Glu Glu Leu Val Gly Thr Asp Lys Lys Leu Pro Gln 460 465 470	1683
GCT GGT AAG TCG GAA GCA ACT CCA CAA CCA GCC ACT TCG GCG TCG CCT Ala Gly Lys Ser Glu Ala Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro 475 480 485 490	1731
AAA CAT GCT TCC ATT TTA GAT GAC GAA CAT CGA AGG AAA GCC TTA CGA Lys His Ala Ser Ile Leu Asp Asp Glu His Arg Arg Lys Ala Leu Arg 495 500 505	1779
AAT AAG ATT CTG GCC GTC GCC AAA GTT TCC AGA ATG TAT TCT GTT CTC Asn Lys Ile Leu Ala Val Ala Lys Val Ser Arg Met Tyr Ser Val Leu 510 515 520	1827
AGA GAA GAA ACC AAT AAA GTT CAG TTT TTA AAA GAT CAC AAT TCA GGC Arg Glu Glu Thr Asn Lys Val Gln Phe Leu Lys Asp His Asn Ser Gly 525 530 535	1875
GTG TTG CCA CGT GGC GCT TTA TCT AAT GGT GTA AAG GGT TTA GAT GAA Val Leu Pro Arg Gly Ala Leu Ser Asn Gly Val Lys Gly Leu Asp Glu 540 545 550	1923
GCC CTG TCT ACC TTT GAA AGG GCA AGA AAG CAC GAT TTA ATT AAT GAA Ala Leu Ser Thr Phe Glu Arg Ala Arg Lys His Asp Leu Ile Asn Glu 555 560 565 570	1971
AAA TTA CCG CCT TCA CTA GAC GAA CTG AAA AAC GAA AAT AAG AAG TAC Lys Leu Pro Pro Ser Leu Asp Glu Leu Lys Asn Glu Asn Lys Lys Tyr 575 580 585	2019
TAC GAA AAA GTT TGG CAG AAA GTA CAT GAA CAT GAT GCA AAG AAT GAT Tyr Glu Lys Val Trp Gln Lys Val His Glu His Asp Ala Lys Asn Asp 590 595 600	2067
AGC AAA TAGAGAAAGC TCCTATTTCC ACTGTACATA CTTCAATAAG TAAGTAAGTT Ser Lys	2123
GCATTAATTA TCTATTTAGA AGCTAGATGC TCCTCAAATG CACAGAATCA TATAGCGTTT	2183
TATTAGGTCT GTTCTTTATT TTAGTTTTGT TGATCTCTAT GAAGGTATAT TTATATGCAA	2243
AAATAAACTT TTAAATATCT ATGGATGCTT ACTCAATTGT ATAGACGTTT TTCATAGGAG	2303
TGCAAATTAT GGACACCACC TTCTAATTGA GCAGAAGCGG TTCTGAATTC	2353

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Ser Asp Ala Ile Arg Asn Thr Glu Gln Ile Asn Ala Ala Ile
 1 5 10 15
 Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro Gln Ser Ser Thr Thr Pro
 20 25 30
 Ile Asp Ser Lys Ala Ser Thr Val Ala Ala Ala Asn Ser Thr Ala Thr
 35 40 45
 Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr Leu Asp Asp Gly Arg Val
 50 55 60
 Val Ser Thr Asn Arg Arg Ile Met Asn Lys Val Pro Ala Ile Thr Ser
 65 70 75 80
 His Val Pro Thr Asp Glu Glu Leu Phe Gln Pro Asn Gly Ile Pro Arg
 85 90 95
 His Glu Phe Leu Arg Asp His Phe Lys Arg Glu Gly Lys Leu Ser Ala
 100 105 110
 Ala Gln Ala Ala Arg Ile Val Thr Leu Ala Thr Glu Leu Phe Ser Lys
 115 120 125
 Glu Pro Asn Leu Ile Ser Val Pro Ala Pro Ile Thr Val Cys Gly Asp
 130 135 140
 Ile His Gly Gln Tyr Phe Asp Leu Leu Lys Leu Phe Glu Val Gly Gly
 145 150 155 160
 Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
 165 170 175
 Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr Ser Leu Lys Leu
 180 185 190
 Asn Phe Asn Asp His Phe Trp Leu Leu Arg Gly Asn His Glu Cys Lys
 195 200 205
 His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met Leu His Lys Tyr
 210 215 220
 Asn Leu Asp Ile Tyr Glu Lys Cys Cys Glu Ser Phe Asn Asn Leu Pro
 225 230 235 240
 Leu Ala Ala Leu Met Asn Gly Gln Tyr Leu Cys Val His Gly Gly Ile
 245 250 255
 Ser Pro Glu Leu Asn Ser Leu Gln Asp Ile Asn Asn Leu Asn Arg Phe
 260 265 270
 Arg Glu Ile Pro Ser His Gly Leu Met Cys Asp Leu Leu Trp Ala Asp
 275 280 285
 Pro Ile Glu Glu Tyr Asp Glu Val Leu Asp Lys Asp Leu Thr Glu Glu
 290 295 300
 Asp Ile Val Asn Ser Lys Thr Met Val Pro His His Gly Lys Met Ala
 305 310 315 320
 Pro Ser Arg Asp Met Phe Val Pro Asn Ser Val Arg Gly Cys Ser Tyr
 325 330 335

60

Ala Phe Thr Tyr Arg Ala Ala Cys His Phe Leu Gln Glu Thr Gly Leu
 340 345 350
 Leu Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met
 355 360 365
 Tyr Lys Asn Thr Lys Thr Leu Gly Phe Pro Ser Leu Leu Thr Leu Phe
 370 375 380
 Ser Ala Pro Asn Tyr Leu Asp Thr Tyr Asn Asn Lys Ala Ala Ile Leu
 385 390 395 400
 Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Met Thr Pro
 405 410 415
 His Pro Tyr Trp Leu Pro Asp Phe Met Asp Val Phe Thr Trp Ser Leu
 420 425 430
 Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Ala Ile Leu Asn
 435 440 445
 Ile Cys Thr Glu Asp Glu Leu Glu Asn Asp Thr Pro Val Ile Glu Glu
 450 455 460
 Leu Val Gly Thr Asp Lys Lys Leu Pro Gln Ala Gly Lys Ser Glu Ala
 465 470 475 480
 Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro Lys His Ala Ser Ile Leu
 485 490 495
 Asp Asp Glu His Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala Val
 500 505 510
 Ala Lys Val Ser Arg Met Tyr Ser Val Leu Arg Glu Glu Thr Asn Lys
 515 520 525
 Val Gln Phe Leu Lys Asp His Asn Ser Gly Val Leu Pro Arg Gly Ala
 530 535 540
 Leu Ser Asn Gly Val Lys Gly Leu Asp Glu Ala Leu Ser Thr Phe Glu
 545 550 555 560
 Arg Ala Arg Lys His Asp Leu Ile Asn Glu Lys Leu Pro Pro Ser Leu
 565 570 575
 Asp Glu Leu Lys Asn Glu Asn Lys Lys Tyr Tyr Glu Lys Val Trp Gln
 580 585 590
 Lys Val His Glu His Asp Ala Lys Asn Asp Ser Lys
 595 600

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: genomic DNA fragment containing full

CNB1 coding sequence

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 54..104

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 181..652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTTGGTAAC TCAATGGTGA TCAGAATCCA TAGAAGCATT TTTATTTCTT AAA ATG	56
Met	
1	
GGT GCT GCT CCT TCC AAA ATT GTG GAT GGT CTT TTA GAA GAT ACA AAT	104
Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr Asn	
5 10 15	
TGTATGTACA CTTCGGAGTG AGGAAAAGAA AGAAACGGGA AATTAACCGA TTTTACTAAC	164
ACTGACACTT TGAACA GTT GAT AGA GAT GAA ATT GAA AGG TTA AGG AAG	213
Val Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys	
1 5 10	
AGA TTC ATG AAA TTA GAT AGA GAT AGC TCA GGG TCT ATT GAT AAA AAT	261
Arg Phe Met Lys Leu Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn	
15 20 25	
GAA TTT ATG AGC ATT CCT GGC GTT TCG TCA AAC CCT CTT GCT GGA CGT	309
Glu Phe Met Ser Ile Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg	
30 35 40	
ATA ATG GAG GTT TTC GAT GCT GAT AAT AGT GGG GAC GTG GAT TTT CAA	357
Ile Met Glu Val Phe Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln	
45 50 55	
GAG TTC ATC ACA GGA TTA TCC ATT TTC AGT GGG CGT GGG TCC AAG GAC	405
Glu Phe Ile Thr Gly Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp	
60 65 70 75	
GAA AAG TTA AGA TTC GCC TTC AAA ATC TAC GAC ATT GAC AAG GAC GGT	453
Glu Lys Leu Arg Phe Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly	
80 85 90	
TTC ATA TCC AAT GGT GAG TTG TTC ATC GTG TTG AAG ATT ATG GTA CGT	501
Phe Ile Ser Asn Gly Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly	
95 100 105	
TCT AAT CTG GAC GAT GAA CAG CTG CAA CAG ATA GTA GAT AGG ACG ATA	549
Ser Asn Leu Asp Asp Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile	
110 115 120	
GTG GAA AAC GAT AGC GAC GGC GAC GGA CGT TTA AGT TTC GAG GAG TTT	597
Val Glu Asn Asp Ser Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe	
125 130 135	
AAG AAT GCT ATC GAA ACC ACA GAA GTG GCC AAG AGT CTG ACA TTG CAA	645
Lys Asn Ala Ile Glu Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln	
140 145 150 155	
TAC GATGTGTAAG ACTAGGGGAC ACTTCATTCA TTTATGGTAT GCCAATATTT	698
Tyr Asp	

TTAAGAAAAG AAGAATAATA CGCGATATTG TTTTAAAGG AAGGAACGCA CACTCGCCCA 758
 GTTAGAGTGC TGATGATATA TACATATATA TATGTATATG TAACAAACAA TAAG 812

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr
 1 5 10 15
 Asn

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys Arg Phe Met Lys Leu
 1 5 10 15
 Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn Glu Phe Met Ser Ile
 20 25 30
 Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg Ile Met Glu Val Phe
 35 40 45
 Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln Glu Phe Ile Thr Gly
 50 55 60
 Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp Glu Lys Leu Arg Phe
 65 70 75 80
 Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly Phe Ile Ser Asn Gly
 85 90 95
 Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly Ser Asn Leu Asp Asp
 100 105 110
 Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile Val Glu Asn Asp Ser
 115 120 125
 Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe Lys Asn Ala Ile Glu
 130 135 140
 Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: coding sequence of CNB1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GGT GCT GCT CCT TCC AAA ATT GTG GAT GGT CTT TTA GAA GAT ACA Met Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr 1 5 10 15	48
AAT TTT GAT AGA GAT GAA ATT GAA AGG TTA AGG AAG AGA TTC ATG AAA Asn Phe Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys Arg Phe Met Lys 20 25 30	96
TTA GAT AGA GAT AGC TCA GGG TCT ATT GAT AAA AAT GAA TTT ATG AGC Leu Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn Glu Phe Met Ser 35 40 45	144
ATT CCT GGC GTT TCG TCA AAC CCT CTT GCT GGA CGT ATA ATG GAG GTT Ile Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg Ile Met Glu Val 50 55 60	192
TTC GAT GCT GAT AAT AGT GGG GAC GTG GAT TTT CAA GAG TTC ATC ACA Phe Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln Glu Phe Ile Thr 65 70 75 80	240
GGA TTA TCC ATT TTC AGT GGG CGT GGG TCC AAG GAC GAA AAG TTA AGA Gly Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp Glu Lys Leu Arg 85 90 95	288
TTC GCC TTC AAA ATC TAC GAC ATT GAC AAG GAC GGT TTC ATA TCC AAT Phe Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly Phe Ile Ser Asn 100 105 110	336
GGT GAG TTG TTC ATC GTG TTG AAG ATT ATG GTA GGT TCT AAT CTG GAC Gly Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly Ser Asn Leu Asp 115 120 125	384
GAT GAA CAG CTG CAA CAG ATA GTA GAT AGG ACG ATA GTG GAA AAC GAT Asp Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile Val Glu Asn Asp 130 135 140	432
AGC GAC GGC GAC GGA CGT TTA AGT TTC GAG GAG TTT AAG AAT GCT ATC Ser Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe Lys Asn Ala Ile 145 150 155 160	480
GAA ACC ACA GAA GTG GCC AAG AGT CTG ACA TTG CAA TAC GAT GT Glu Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln Tyr Asp 165 170	524

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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Met Gly Ala Ala Pro Ser Lys Ile Val Asp Gly Leu Leu Glu Asp Thr
 1           5           10           15
Asn Phe Asp Arg Asp Glu Ile Glu Arg Leu Arg Lys Arg Phe Met Lys
      20           25           30
Leu Asp Arg Asp Ser Ser Gly Ser Ile Asp Lys Asn Glu Phe Met Ser
      35           40           45
Ile Pro Gly Val Ser Ser Asn Pro Leu Ala Gly Arg Ile Met Glu Val
      50           55           60
Phe Asp Ala Asp Asn Ser Gly Asp Val Asp Phe Gln Glu Phe Ile Thr
      65           70           75           80
Gly Leu Ser Ile Phe Ser Gly Arg Gly Ser Lys Asp Glu Lys Leu Arg
      85           90           95
Phe Ala Phe Lys Ile Tyr Asp Ile Asp Lys Asp Gly Phe Ile Ser Asn
      100          105          110
Gly Glu Leu Phe Ile Val Leu Lys Ile Met Val Gly Ser Asn Leu Asp
      115          120          125
Asp Glu Gln Leu Gln Gln Ile Val Asp Arg Thr Ile Val Glu Asn Asp
      130          135          140
Ser Asp Gly Asp Gly Arg Leu Ser Phe Glu Glu Phe Lys Asn Ala Ile
      145          150          155          160
Glu Thr Thr Glu Val Ala Lys Ser Leu Thr Leu Gln Tyr Asp
      165          170

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: DNA fragment containing CNAldeltaC coding sequence

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 286..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTTGTTGCA TTTTGATATT CATCTATATC TATTTCAAAA TTTTTCATGT CATCGCCTCT	60
TGAAACATGA ATTTTCCAAT TCTGAAAAAG AACGTACTAC TGGGAAACAA AAGGGAAAAA	120
TGTATAAATC CTTTAATGTT TTTGAATCAA GAGGCATTAT TATAAAAGAA CGAAGCAAAG	180
CCTTTAATAT TTGCTTTATT AAAGGTATTA TTCAAAGAAA AGTTTTTTTA GATTCTTTT	240
TTTTTGACGT ATTAGCTCAG CTGCCATAAA ACACTCTCAA CGCCA ATG TCG AAA	294
Met Ser Lys	
1	
GAC TTG AAT TCT TCA CGC ATC AAA ATC ATT AAA CCT AAT GAC TCT TAC	342
Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn Asp Ser Tyr	
5 10 15	
ATA AAG GTT GAC CGG AAA AAA GAT TTA ACA AAA TAC GAA TTA GAA AAC	390
Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu Leu Glu Asn	
20 25 30 35	
GGT AAA GTA ATT TCT ACT AAG GAC CGA TCC TAC GCT TCT GTA CCT GCC	438
Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser Val Pro Ala	
40 45 50	
ATA ACA GGA AAG ATA CCA AGT GAT GAG GAA GTA TTC GAC TCC AAG ACG	486
Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp Ser Lys Thr	
55 60 65	
GGA TTA CCT AAT CAT TCC TTT TTA AGA GAG CAT TTC TTT CAT GAG GGT	534
Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe His Glu Gly	
70 75 80	
CGA CTT TCT AAG GAA CAG GCC ATA AAA ATC TTA AAT ATG TCA ACT GTA	582
Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met Ser Thr Val	
85 90 95	
GCA TTG AGT AAA GAA CCC AAT CTA CTA AAA CTC AAA GCG CCA ATT ACT	630
Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala Pro Ile Thr	
100 105 110 115	
ATA TGT GGT GAT ATT CAC GGG CAG TAT TAT GAT TTA TTG AAA CTG TTT	678
Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu Lys Leu Phe	
120 125 130	
GAA GTT GGC GGT GAC CCC GCC GAA ATC GAC TAT TTA TTC TTG GGG GAT	726
Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe Leu Gly Asp	
135 140 145	
TAT GTT GAT AGA GGT GCA TTC TCT TTT GAG TGT CTG ATT TAT TTG TAC	774
Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr	
150 155 160	
TCC TTG AAG TTG AAT AAT TTA GGG AGA TTT TGG ATG CTA AGA GGT AAC	822
Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu Arg Gly Asn	
165 170 175	
CAT GAG TGT AAG CAC TTG ACC TCT TAT TTT ACT TTT AAG AAT GAG ATG	870
His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met	
180 185 190 195	
TTG CAC AAA TAC GAT ATG GAA GTT TAC GAT GCT TGC TGC AGA TCA TTC	918
Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys Arg Ser Phe	
200 205 210	

AAT	GTC	TTA	CCA	TTA	GCA	GCT	TTA	ATG	AAC	GGA	CAA	TAT	TTT	TGT	GTG	966
Asn	Val	Leu	Pro	Leu	Ala	Ala	Leu	Met	Asn	Gly	Gln	Tyr	Phe	Cys	Val	
			215					220					225			
CAT	GGT	GGT	ATC	TCT	CCA	GAG	TTA	AAA	TCA	GTA	GAG	GAT	GTT	AAT	AAA	1014
His	Gly	Gly	Ile	Ser	Pro	Glu	Leu	Lys	Ser	Val	Glu	Asp	Val	Asn	Lys	
		230					235					240				
ATT	AAT	AGA	TTT	CGA	GAA	ATC	CCA	TCT	CGT	GGT	CTC	ATG	TGT	GAC	CTA	1062
Ile	Asn	Arg	Phe	Arg	Glu	Ile	Pro	Ser	Arg	Gly	Leu	Met	Cys	Asp	Leu	
	245					250					255					
CTA	TGG	GCC	GAT	CCT	GTC	GAA	AAT	TAT	GAT	GAT	GCA	AGA	GAT	GGT	AGC	1110
Leu	Trp	Ala	Asp	Pro	Val	Glu	Asn	Tyr	Asp	Asp	Ala	Arg	Asp	Gly	Ser	
260					265				270						275	
GAA	TTT	GAT	CAG	AGC	GAG	GAT	GAA	TTC	GTA	CCT	AAC	AGT	TTG	AGG	GGT	1158
Glu	Phe	Asp	Gln	Ser	Glu	Asp	Glu	Phe	Val	Pro	Asn	Ser	Leu	Arg	Gly	
				280					285					290		
TGC	TCT	TTC	GCC	TTC	ACT	TTT	AAA	GCA	TCA	TGC	AAG	TTT	TTG	AAG	GCA	1206
Cys	Ser	Phe	Ala	Phe	Thr	Phe	Lys	Ala	Ser	Cys	Lys	Phe	Leu	Lys	Ala	
			295					300					305			
AAT	GGT	TTG	TTA	TCT	ATT	ATT	AGA	GCA	CAC	GAA	GCA	CAG	GAT	GCT	GGG	1254
Asn	Gly	Leu	Leu	Ser	Ile	Ile	Arg	Ala	His	Glu	Ala	Gln	Asp	Ala	Gly	
		310					315					320				
TAC	AGA	ATG	TAT	AAA	AAC	AAT	AAA	GTA	ACA	GGC	TTC	CCG	AGC	TTA	ATA	1302
Tyr	Arg	Met	Tyr	Lys	Asn	Asn	Lys	Val	Thr	Gly	Phe	Pro	Ser	Leu	Ile	
	325					330					335					
ACC	ATG	TTC	AGT	GCG	CCA	AAC	TAC	CTG	GAC	ACA	TAT	CAT	AAT	AAA	GCT	1350
Thr	Met	Phe	Ser	Ala	Pro	Asn	Tyr	Leu	Asp	Thr	Tyr	His	Asn	Lys	Ala	
340					345				350						355	
GCT	GTG	TTA	AAA	TAT	GAA	GAA	AAC	GTC	ATG	AAC	ATC	AGG	CAG	TTT	CAC	1398
Ala	Val	Leu	Lys	Tyr	Glu	Glu	Asn	Val	Met	Asn	Ile	Arg	Gln	Phe	His	
				360				365						370		
ATG	TCT	CCG	CAC	CCT	TAC	TGG	TTG	CCT	GAT	TTT	ATG	GAT	GTT	TTC	ACC	1446
Met	Ser	Pro	His	Pro	Tyr	Trp	Leu	Pro	Asp	Phe	Met	Asp	Val	Phe	Thr	
			375					380					385			
TGG	TCA	CTA	CCT	TTT	GTT	GGC	GAA	AAA	GTT	ACT	AGC	ATG	TTA	GTG	TCT	1494
Trp	Ser	Leu	Pro	Phe	Val	Gly	Glu	Lys	Val	Thr	Ser	Met	Leu	Val	Ser	
		390					395					400				
ATA	TTA	AAC	ATA	TGT	AGT	GAG	CAG	GAA	CTT	GAC	CCA	GAA	TCG	GAA	CCC	1542
Ile	Leu	Asn	Ile	Cys	Ser	Glu	Gln	Glu	Leu	Asp	Pro	Glu	Ser	Glu	Pro	
	405					410					415					
AAA	GCT	GCG	GAG	GAG	ACT	GTA	AAG	GCA	AGA	GCA	AAC	GCA	ACT	AAG	GAG	1590
Lys	Ala	Ala	Glu	Glu	Thr	Val	Lys	Ala	Arg	Ala	Asn	Ala	Thr	Lys	Glu	
420					425				430						435	
ACC	GGC	ACC	CCA	TCT	GAT	GAA	AAG	GCG	TCA	TCA	GCG	ATA	TTA	GAA	GAT	1638
Thr	Gly	Thr	Pro	Ser	Asp	Glu	Lys	Ala	Ser	Ser	Ala	Ile	Leu	Glu	Asp	
				440				445						450		
GAA	ACC	CGA	AGA	AAG	GCT	TTG	AGA	AAT	AAG	ATA	TTA	GCT	ATT	GCT	AAA	1686
Glu	Thr	Arg	Arg	Lys	Ala	Leu	Arg	Asn	Lys	Ile	Leu	Ala	Ile	Ala	Lys	
			455					460					465			
GTT	TCA	AGA	ATG	TTT	TCG	GTG	CTA	AGA	GAA	GAG	AGC	GAA	AAA	GTG	GAA	1734
Val	Ser	Arg	Met	Phe	Ser	Val	Leu	Arg	Glu	Glu	Ser	Glu	Lys	Val	Glu	
		470					475					480				

67

TAT TTG AAA ACT ATG AAT GCC GGT GTC TTA CCT CGT GGT GCT CTA GCT 1782
 Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly Ala Leu Ala
 485 490 495

CGT GGG ACT GAA GGT TTG AAT GAA ACG CTA 1812
 Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu
 500 505

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Lys Asp Leu Asn Ser Ser Arg Ile Lys Ile Ile Lys Pro Asn
 1 5 10 15
 Asp Ser Tyr Ile Lys Val Asp Arg Lys Lys Asp Leu Thr Lys Tyr Glu
 20 25 30
 Leu Glu Asn Gly Lys Val Ile Ser Thr Lys Asp Arg Ser Tyr Ala Ser
 35 40 45
 Val Pro Ala Ile Thr Gly Lys Ile Pro Ser Asp Glu Glu Val Phe Asp
 50 55 60
 Ser Lys Thr Gly Leu Pro Asn His Ser Phe Leu Arg Glu His Phe Phe
 65 70 75 80
 His Glu Gly Arg Leu Ser Lys Glu Gln Ala Ile Lys Ile Leu Asn Met
 85 90 95
 Ser Thr Val Ala Leu Ser Lys Glu Pro Asn Leu Leu Lys Leu Lys Ala
 100 105 110
 Pro Ile Thr Ile Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu
 115 120 125
 Lys Leu Phe Glu Val Gly Gly Asp Pro Ala Glu Ile Asp Tyr Leu Phe
 130 135 140
 Leu Gly Asp Tyr Val Asp Arg Gly Ala Phe Ser Phe Glu Cys Leu Ile
 145 150 155 160
 Tyr Leu Tyr Ser Leu Lys Leu Asn Asn Leu Gly Arg Phe Trp Met Leu
 165 170 175
 Arg Gly Asn His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys
 180 185 190
 Asn Glu Met Leu His Lys Tyr Asp Met Glu Val Tyr Asp Ala Cys Cys
 195 200 205
 Arg Ser Phe Asn Val Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr
 210 215 220
 Phe Cys Val His Gly Gly Ile Ser Pro Glu Leu Lys Ser Val Glu Asp
 225 230 235 240
 Val Asn Lys Ile Asn Arg Phe Arg Glu Ile Pro Ser Arg Gly Leu Met
 245 250 255

68

Cys Asp Leu Leu Trp Ala Asp Pro Val Glu Asn Tyr Asp Asp Ala Arg
 260 265 270
 Asp Gly Ser Glu Phe Asp Gln Ser Glu Asp Glu Phe Val Pro Asn Ser
 275 280 285
 Leu Arg Gly Cys Ser Phe Ala Phe Thr Phe Lys Ala Ser Cys Lys Phe
 290 295 300
 Leu Lys Ala Asn Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln
 305 310 315 320
 Asp Ala Gly Tyr Arg Met Tyr Lys Asn Asn Lys Val Thr Gly Phe Pro
 325 330 335
 Ser Leu Ile Thr Met Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr His
 340 345 350
 Asn Lys Ala Ala Val Leu Lys Tyr Glu Glu Asn Val Met Asn Ile Arg
 355 360 365
 Gln Phe His Met Ser Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp
 370 375 380
 Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Ser Met
 385 390 395 400
 Leu Val Ser Ile Leu Asn Ile Cys Ser Glu Gln Glu Leu Asp Pro Glu
 405 410 415
 Ser Glu Pro Lys Ala Ala Glu Glu Thr Val Lys Ala Arg Ala Asn Ala
 420 425 430
 Thr Lys Glu Thr Gly Thr Pro Ser Asp Glu Lys Ala Ser Ser Ala Ile
 435 440 445
 Leu Glu Asp Glu Thr Arg Arg Lys Ala Leu Arg Asn Lys Ile Leu Ala
 450 455 460
 Ile Ala Lys Val Ser Arg Met Phe Ser Val Leu Arg Glu Glu Ser Glu
 465 470 475 480
 Lys Val Glu Tyr Leu Lys Thr Met Asn Ala Gly Val Leu Pro Arg Gly
 485 490 495
 Ala Leu Ala Arg Gly Thr Glu Gly Leu Asn Glu Thr Leu
 500 505

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: DNA fragment containing CNA2deltaC coding sequence

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 262..1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGTCTATA ATACGTTTGA TACAGCTAGA TATCGCTAGC GCCAACATTG TCCCCCTCTC	60
TTGATCAATG CTTTTTTTCG GCCCGAGACA AATGAGAAAA TGTCTTAAAA ATACCTTTCA	120
TCAAGACTCC TATTTTTCCT TAGAAAAAAC ATATATCCAA CTGGAACAGT ATTAAGCCAA	180
TTGCTACGAT ACAAACAAAA GGAGATATTC CTTCCCTCCC ATAGAGTCAC ACAGGAGCCA	240
GTACTTCTTC TTGAACCCGC A ATG TCT TCA GAC GCT ATA AGA AAT ACT GAG	291
Met Ser Ser Asp Ala Ile Arg Asn Thr Glu	10
CAG ATA AAC GCC GCT ATT AAA ATT ATA GAA AAC AAA ACA GAG CGT CCG	339
Gln Ile Asn Ala Ala Ile Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro	25
CAA TCG TCC ACA ACC CCT ATA GAT TCG AAG GCT AGT ACA GTT GCT GCT	387
Gln Ser Ser Thr Thr Pro Ile Asp Ser Lys Ala Ser Thr Val Ala Ala	40
GCT AAT TCC ACG GCC ACA GAA ACT TCC AGA GAC CTT ACA CAA TAT ACC	435
Ala Asn Ser Thr Ala Thr Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr	55
CTA GAT GAC GGA AGA GTC GTA TCG ACA AAC CGC AGA ATA ATG AAT AAA	483
Leu Asp Asp Gly Arg Val Val Ser Thr Asn Arg Arg Ile Met Asn Lys	70
GTG CCC GCC ATC ACG TCA CAT GTT CCT ACA GAT GAA GAG CTG TTC CAG	531
Val Pro Ala Ile Thr Ser His Val Pro Thr Asp Glu Glu Leu Phe Gln	90
CCC AAT GGG ATA CCT CGT CAC GAA TTC CTA AGA GAT CAT TTC AAG CGC	579
Pro Asn Gly Ile Pro Arg His Glu Phe Leu Arg Asp His Phe Lys Arg	105
GAG GGC AAA TTG TCG GCT GCG CAG GCG GCC AGG ATC GTT ACA CTT GCA	627
Glu Gly Lys Leu Ser Ala Ala Gln Ala Ala Arg Ile Val Thr Leu Ala	120
ACG GAA CTC TTC AGC AAA GAA CCC AAC CTT ATA TCT GTT CCC GCC CCA	675
Thr Glu Leu Phe Ser Lys Glu Pro Asn Leu Ile Ser Val Pro Ala Pro	135
ATC ACA GTT TGC GGT GAT ATC CAT GGC CAG TAC TTT GAC CTT TTG AAG	723
Ile Thr Val Cys Gly Asp Ile His Gly Gln Tyr Phe Asp Leu Leu Lys	150
CTA TTC GAA GTT GGC GGA GAT CCG GCC ACT ACA TCG TAT TTG TTC TTG	771
Leu Phe Glu Val Gly Gly Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu	170
GGA GAC TAT GTC GAC AGA GGG TCC TTT TCG TTT GAG TGT CTT ATT TAT	819
Gly Asp Tyr Val Asp Arg Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr	185
TTA TAT TCT TTG AAG CTG AAT TTT AAC GAC CAT TTC TGG CTA CTG AGG	867
Leu Tyr Ser Leu Lys Leu Asn Phe Asn Asp His Phe Trp Leu Leu Arg	200

GGT AAC CAC GAA TGT AAG CAT CTA ACG TCA TAT TTC ACT TTC AAA AAT Gly Asn His Glu Cys Lys His Leu Thr Ser Tyr Phe Thr Phe Lys Asn 205 210 215	915
GAA ATG CTG CAC AAG TAC AAT CTA GAT ATT TAC GAG AAA TGC TGC GAA Glu Met Leu His Lys Tyr Asn Leu Asp Ile Tyr Glu Lys Cys Cys Glu 220 225 230	963
TCG TTT AAC AAC TTG CCC CTG GCT GCG TTA ATG AAC GGA CAG TAT CTT Ser Phe Asn Asn Leu Pro Leu Ala Ala Leu Met Asn Gly Gln Tyr Leu 235 240 245 250	1011
TGT GTT CAT GGT GGT ATA TCT CCC GAG TTA AAC TCT TTA CAG GAC ATT Cys Val His Gly Gly Ile Ser Pro Glu Leu Asn Ser Leu Gln Asp Ile 255 260 265	1059
AAC AAC CTA AAT AGA TTC AGG GAG ATT CCC TCT CAT GGC CTG ATG TGT Asn Asn Leu Asn Arg Phe Arg Glu Ile Pro Ser His Gly Leu Met Cys 270 275 280	1107
GAT CTG TTG TGG GCT GAC CCG ATT GAA GAG TAC GAC GAA GTC TTG GAT Asp Leu Leu Trp Ala Asp Pro Ile Glu Glu Tyr Asp Glu Val Leu Asp 285 290 295	1155
AAA GAC TTG ACT GAG GAA GAC ATA GTG AAC TCC AAA ACC ATG GTT CCT Lys Asp Leu Thr Glu Glu Asp Ile Val Asn Ser Lys Thr Met Val Pro 300 305 310	1203
CAT CAT GGC AAG ATG GCA CCT TCA AGG GAT ATG TTT GTC CCA AAC TCA His His Gly Lys Met Ala Pro Ser Arg Asp Met Phe Val Pro Asn Ser 315 320 325 330	1251
GTA AGG GGC TGT TCA TAT GCC TTC ACG TAT CGT GCT GCG TGC CAT TTT Val Arg Gly Cys Ser Tyr Ala Phe Thr Tyr Arg Ala Ala Cys His Phe 335 340 345	1299
CTG CAA GAG ACT GGC CTG TTG TCC ATC ATC AGG GCA CAC GAG GCT CAA Leu Gln Glu Thr Gly Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln 350 355 360	1347
GAC GCT GGT TAT AGA ATG TAC AAA AAT ACC AAG ACT TTG GGC TTT CCC Asp Ala Gly Tyr Arg Met Tyr Lys Asn Thr Lys Thr Leu Gly Phe Pro 365 370 375	1395
TCT CTT TTG ACC CTT TTC AGT GCG CCT AAC TAC TTG GAC ACC TAC AAT Ser Leu Leu Thr Leu Phe Ser Ala Pro Asn Tyr Leu Asp Thr Tyr Asn 380 385 390	1443
AAT AAG GCT GCC ATA TTG AAA TAC GAA AAT AAT GTT ATG AAT ATC AGA Asn Lys Ala Ala Ile Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg 395 400 405 410	1491
CAA TTC AAC ATG ACT CCA CAC CCC TAT TGG TTA CCA GAT TTC ATG GAC Gln Phe Asn Met Thr Pro His Pro Tyr Trp Leu Pro Asp Phe Met Asp 415 420 425	1539
GTT TTC ACG TGG TCC TTG CCA TTT GTT GGT GAA AAA GTT ACA GAG ATG Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met 430 435 440	1587
CTT GTC GCA ATT CTA AAC ATC TGT ACT GAA GAT GAG CTG GAA AAC GAC Leu Val Ala Ile Leu Asn Ile Cys Thr Glu Asp Glu Leu Glu Asn Asp 445 450 455	1635
ACC CCC GTC ATT GAA GAA TTA GTT GGT ACC GAT AAA AAA TTG CCA CAA Thr Pro Val Ile Glu Glu Leu Val Gly Thr Asp Lys Lys Leu Pro Gln 460 465 470	1683

GCT GGT AAG TCG GAA GCA ACT CCA CAA CCA GCC ACT TCG GCG TCG CCT 1731
 Ala Gly Lys Ser Glu Ala Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro
 475 480 485 490

AAA CAT GCT TCC ATT TTA GAT GAC GAA CAT CGA AGG 1767
 Lys His Ala Ser Ile Leu Asp Asp Glu His Arg Arg
 495 500

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Ser Asp Ala Ile Arg Asn Thr Glu Gln Ile Asn Ala Ala Ile
 1 5 10 15
 Lys Ile Ile Glu Asn Lys Thr Glu Arg Pro Gln Ser Ser Thr Thr Pro
 20 25 30
 Ile Asp Ser Lys Ala Ser Thr Val Ala Ala Ala Asn Ser Thr Ala Thr
 35 40 45
 Glu Thr Ser Arg Asp Leu Thr Gln Tyr Thr Leu Asp Asp Gly Arg Val
 50 55 60
 Val Ser Thr Asn Arg Arg Ile Met Asn Lys Val Pro Ala Ile Thr Ser
 65 70 75 80
 His Val Pro Thr Asp Glu Glu Leu Phe Gln Pro Asn Gly Ile Pro Arg
 85 90 95
 His Glu Phe Leu Arg Asp His Phe Lys Arg Glu Gly Lys Leu Ser Ala
 100 105 110
 Ala Gln Ala Ala Arg Ile Val Thr Leu Ala Thr Glu Leu Phe Ser Lys
 115 120 125
 Glu Pro Asn Leu Ile Ser Val Pro Ala Pro Ile Thr Val Cys Gly Asp
 130 135 140
 Ile His Gly Gln Tyr Phe Asp Leu Leu Lys Leu Phe Glu Val Gly Gly
 145 150 155 160
 Asp Pro Ala Thr Thr Ser Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
 165 170 175
 Gly Ser Phe Ser Phe Glu Cys Leu Ile Tyr Leu Tyr Ser Leu Lys Leu
 180 185 190
 Asn Phe Asn Asp His Phe Trp Leu Leu Arg Gly Asn His Glu Cys Lys
 195 200 205
 His Leu Thr Ser Tyr Phe Thr Phe Lys Asn Glu Met Leu His Lys Tyr
 210 215 220
 Asn Leu Asp Ile Tyr Glu Lys Cys Cys Glu Ser Phe Asn Asn Leu Pro
 225 230 235 240
 Leu Ala Ala Leu Met Asn Gly Gln Tyr Leu Cys Val His Gly Gly Ile
 245 250 255

Ser Pro Glu Leu Asn Ser Leu Gln Asp Ile Asn Asn Leu Asn Arg Phe
 260 265 270
 Arg Glu Ile Pro Ser His Gly Leu Met Cys Asp Leu Leu Trp Ala Asp
 275 280 285
 Pro Ile Glu Glu Tyr Asp Glu Val Leu Asp Lys Asp Leu Thr Glu Glu
 290 295 300
 Asp Ile Val Asn Ser Lys Thr Met Val Pro His His Gly Lys Met Ala
 305 310 315 320
 Pro Ser Arg Asp Met Phe Val Pro Asn Ser Val Arg Gly Cys Ser Tyr
 325 330 335
 Ala Phe Thr Tyr Arg Ala Ala Cys His Phe Leu Gln Glu Thr Gly Leu
 340 345 350
 Leu Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met
 355 360 365
 Tyr Lys Asn Thr Lys Thr Leu Gly Phe Pro Ser Leu Leu Thr Leu Phe
 370 375 380
 Ser Ala Pro Asn Tyr Leu Asp Thr Tyr Asn Asn Lys Ala Ala Ile Leu
 385 390 395 400
 Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Met Thr Pro
 405 410 415
 His Pro Tyr Trp Leu Pro Asp Phe Met Asp Val Phe Thr Trp Ser Leu
 420 425 430
 Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Ala Ile Leu Asn
 435 440 445
 Ile Cys Thr Glu Asp Glu Leu Glu Asn Asp Thr Pro Val Ile Glu Glu
 450 455 460
 Leu Val Gly Thr Asp Lys Lys Leu Pro Gln Ala Gly Lys Ser Glu Ala
 465 470 475 480
 Thr Pro Gln Pro Ala Thr Ser Ala Ser Pro Lys His Ala Ser Ile Leu
 485 490 495
 Asp Asp Glu His Arg Arg
 500

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: G4-PCR-A

73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCCTATCGT GCACTCACCG ACGC

24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: G4-PCR-B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGAAGGCCC TACTGAGCCA GGAG

24

IT IS CLAIMED:

1. A polypeptide composition comprising a polypeptide effective to enhance immunosuppressive effects of a calcineurin-targeted immunosuppressant by potentiating an interaction of an immunophilin with calcineurin.
5
2. A composition of claim 1, wherein the polypeptide composition contains a calcineurin interacting (CNI) polypeptide.
- 10 3. A composition of claim 2, wherein the polypeptide composition contains a polypeptide having an amino acid sequence selected from the group consisting of sequences represented by SEQ ID NO:2 and SEQ ID NO:5.
4. A composition of claim 2, wherein the polypeptide has an amino acid sequence of
15 between 15 and 915 amino acids in length.
5. A composition of claim 2, wherein the polypeptide composition contains a polypeptide having an amino acid sequence comprising the c-terminal 306 amino acids of a CNI protein.
20
6. An isolated nucleic acid having a sequence encoding a polypeptide of any of claims 1-5.
7. A nucleic acid of claim 6, wherein the nucleic acid has a sequence selected from
25 the group consisting of nucleic acid sequences represented by SEQ ID NO:3 and SEQ ID NO:6.
8. A method of identifying a small molecule immunosuppressant compound, comprising
30 constructing a cell-based two hybrid protein-protein interaction assay, wherein one of two fusion hybrid proteins in a cell contains an (A) subunit of calcineurin, and the other of two fusion hybrid proteins contains a CNI polypeptide,
contacting the cell with a small molecule, and

identifying the small molecule as an immunosuppressant if the molecule potentiates an interaction between the two hybrid proteins.

9. A method of claim 8, wherein the cell is a yeast cell.

5

10. A method of claim 8, wherein one of the two fusion hybrid proteins contains a GAL4 activation domain and the other of two fusion hybrid proteins contains a GAL4 binding domain.

10

11. A method of claim 8, wherein the subunit of calcineurin is selected from the group consisting of yeast CNA1 and yeast CNA2.

12. A method of claim 8, wherein the subunit of calcineurin is an "A" subunit of human calcineurin.

15

13. A method of claim 8, wherein the CNI polypeptide is yeast CNI polypeptide.

14. A method of claim 8, wherein the CNI polypeptide is yeast CN1c polypeptide.

20

15. A method of claim 8, wherein the cell is further modified to cause overexpression of a "B" subunit of calcineurin by said cell.

16. A yeast cell carrying a mutation in the naturally-occurring genomic copy of a gene encoding calcineurin-interacting polypeptide, where said mutation prevents expression of a functional calcineurin-interacting polypeptide from said genomic copy.

25

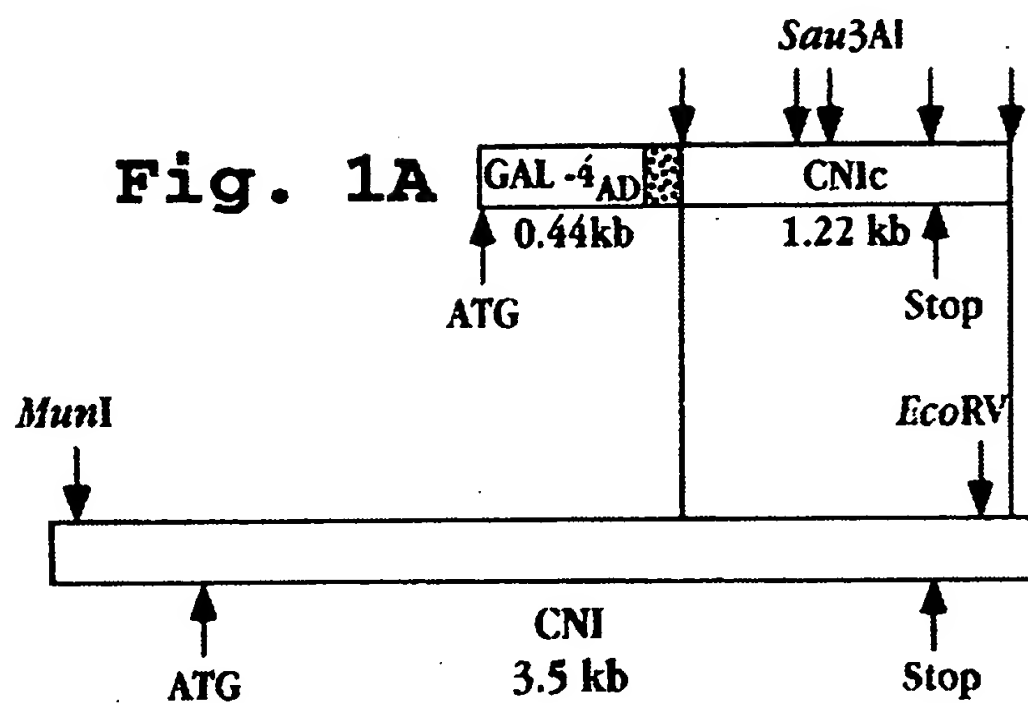


Fig. 1B

Fig. 2A

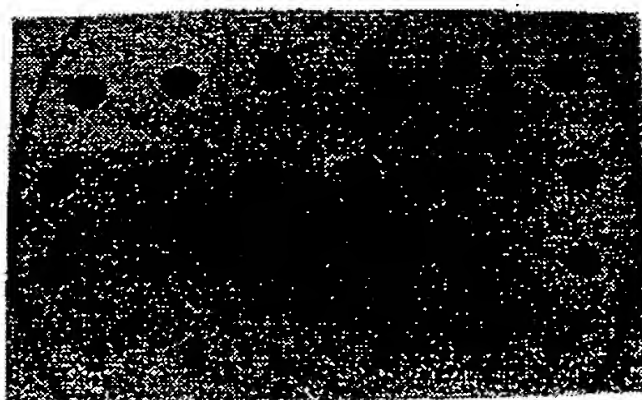
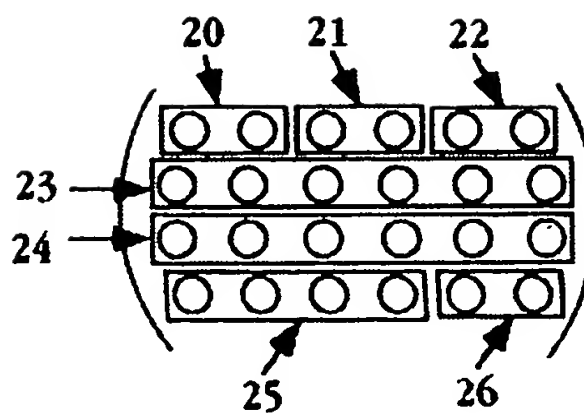


Fig. 2B



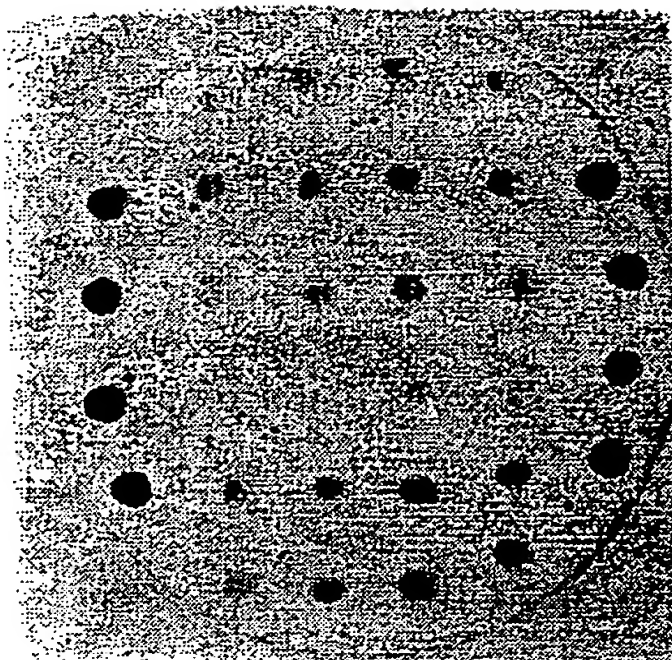


Fig. 3A

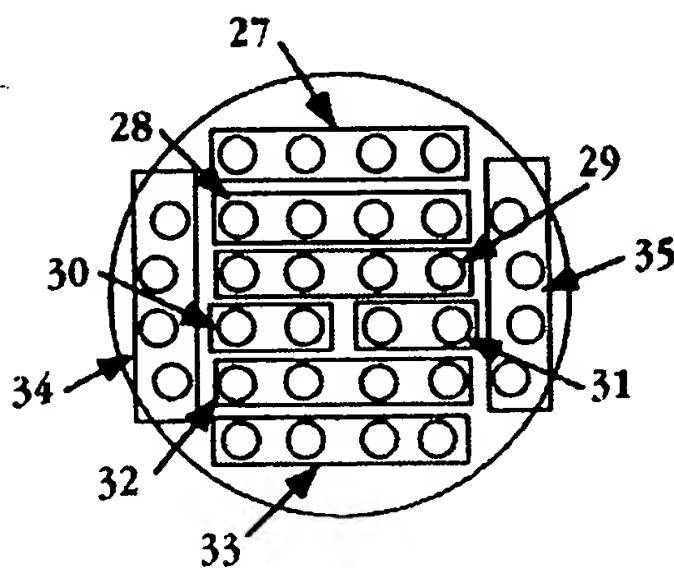


Fig. 3B

3/1.1

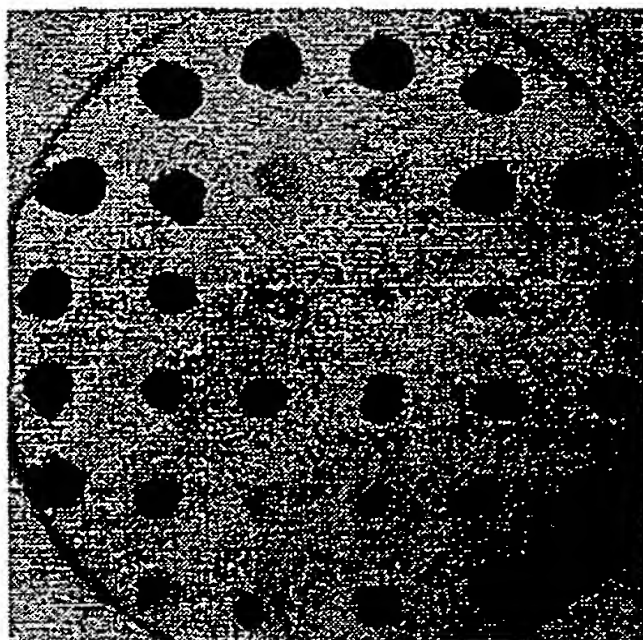


Fig. 4A

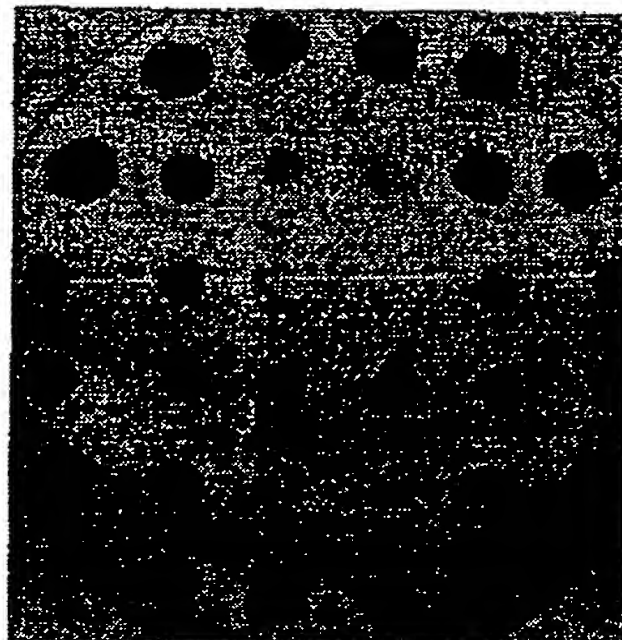


Fig. 4C

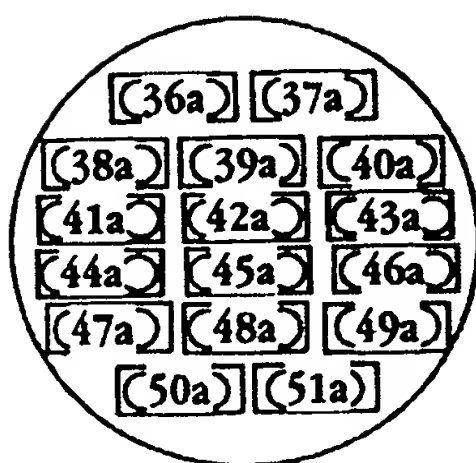


Fig. 4B

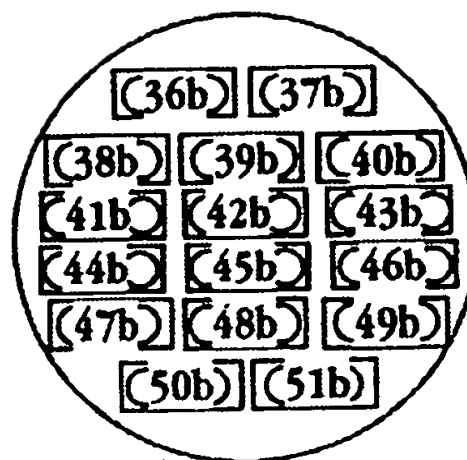


Fig. 4D

SUBSTITUTE SHEET (RULE 26)

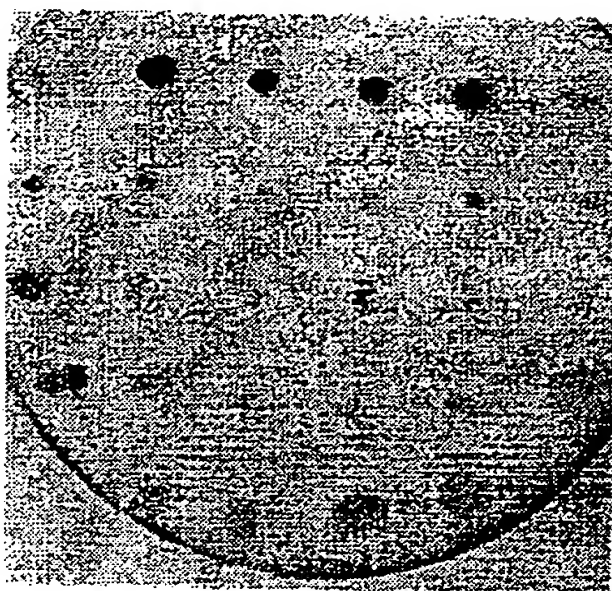


Fig. 5A

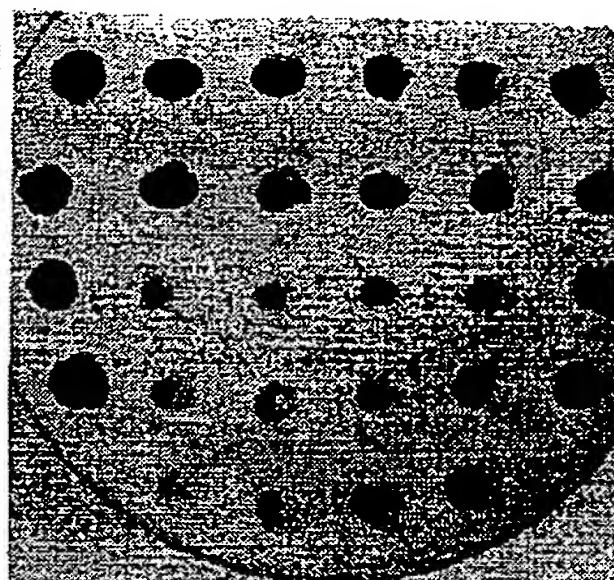


Fig. 5C

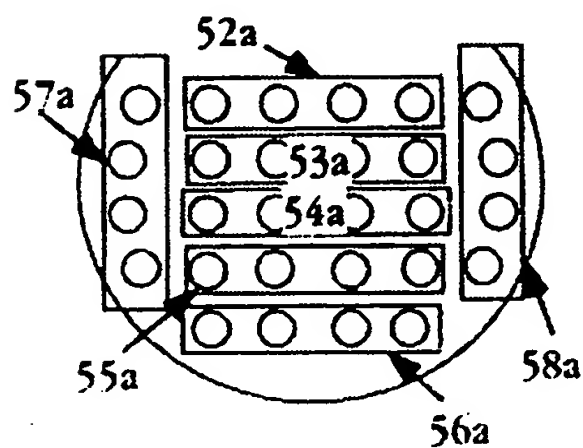


Fig. 5B

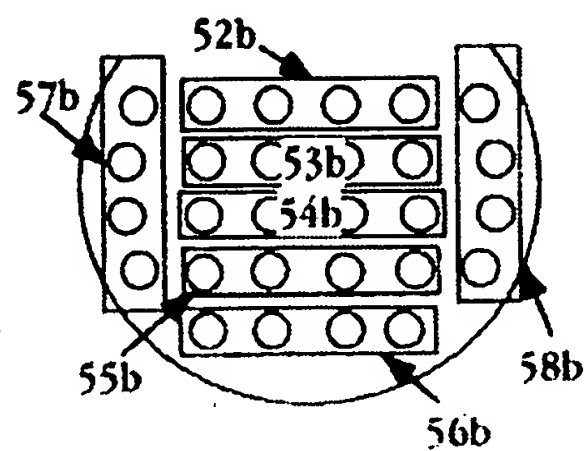


Fig. 5D

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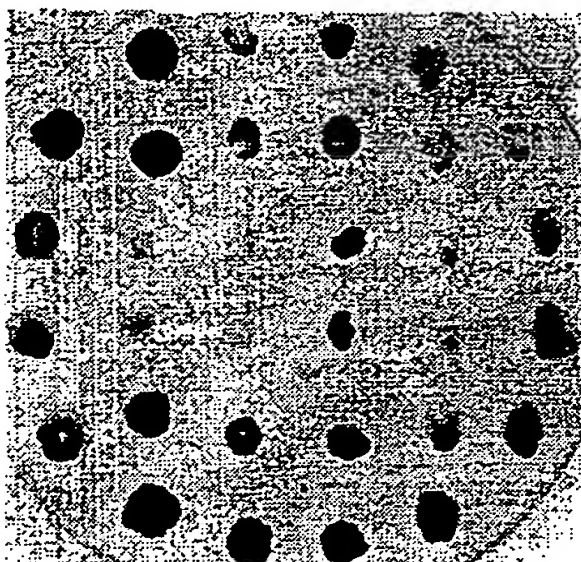


Fig. 6E

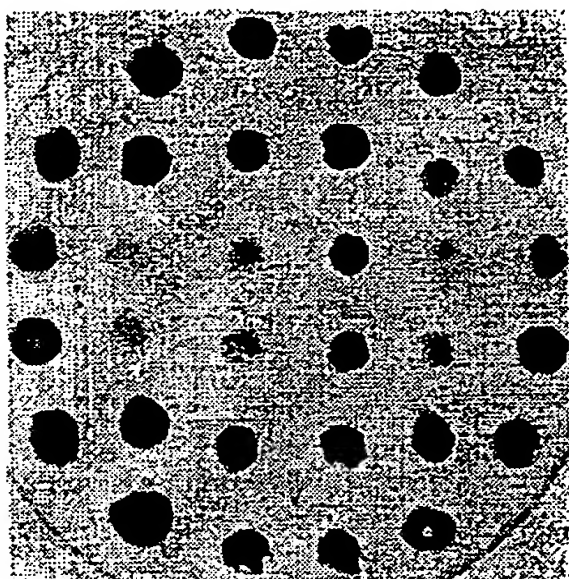


Fig. 6C

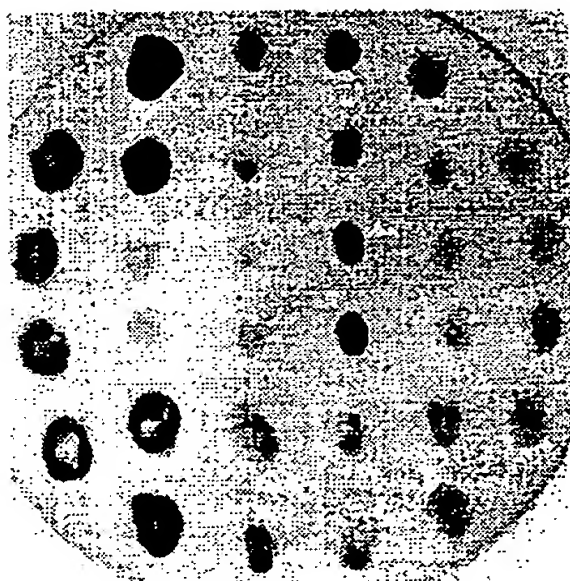


Fig. 6A

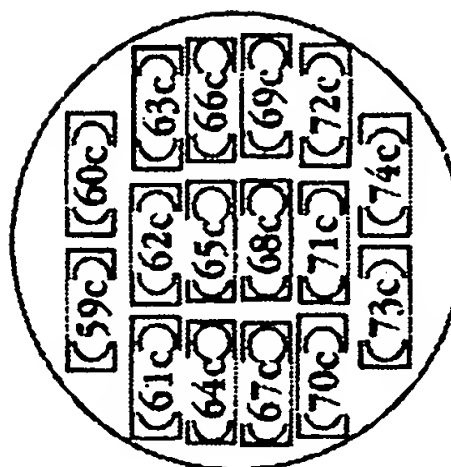


Fig. 6F

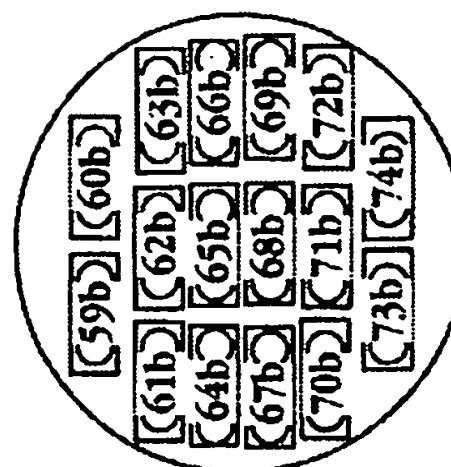


Fig. 6D

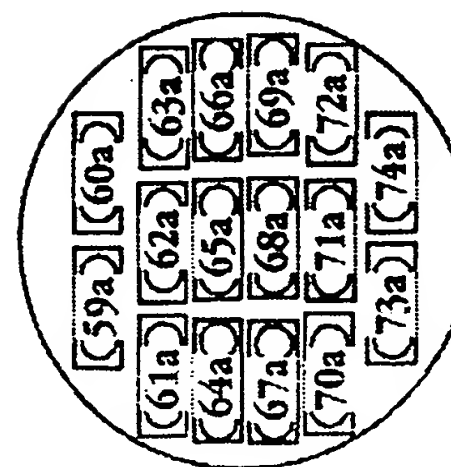


Fig. 6B

6/11

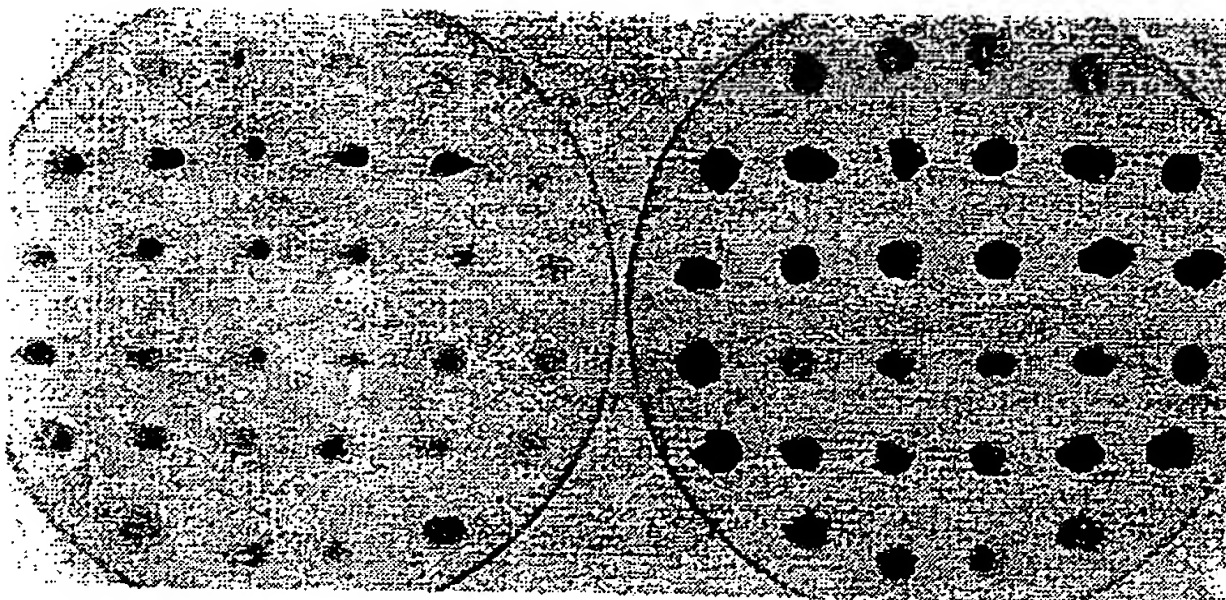


Fig. 7A

Fig. 7C

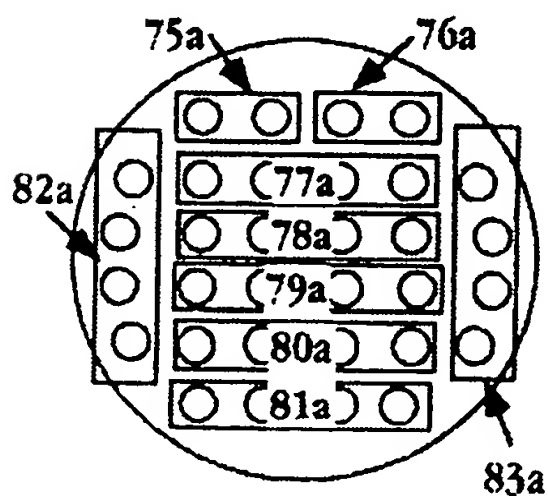


Fig. 7B

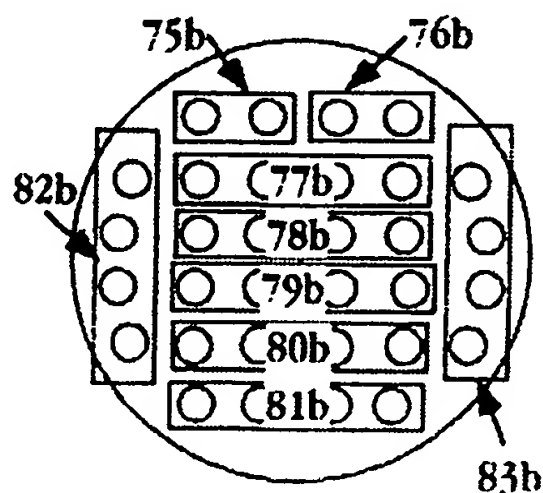


Fig. 7D

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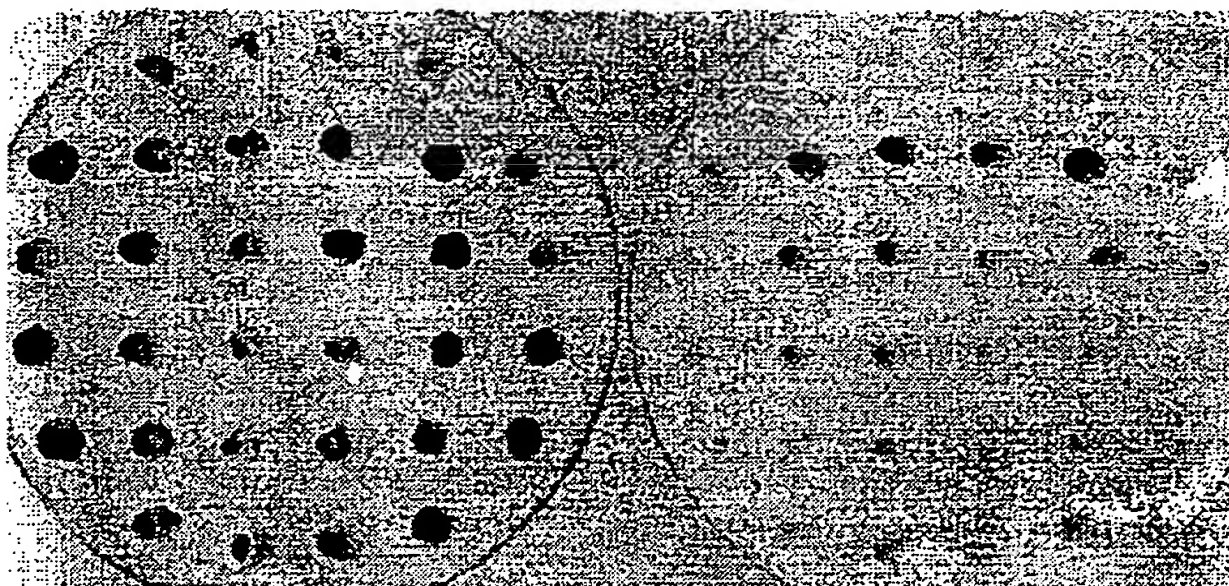


Fig. 7E

Fig. 7G

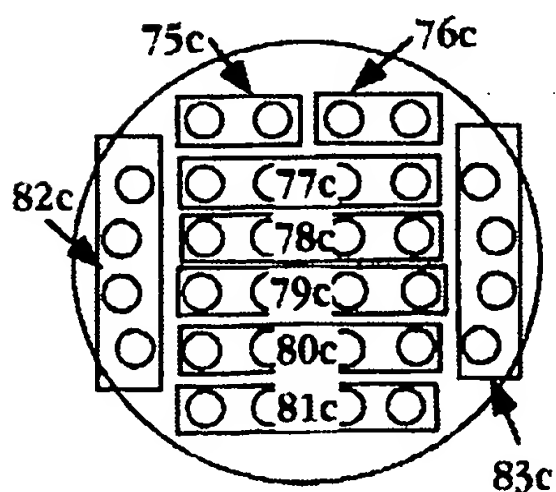


Fig. 7F

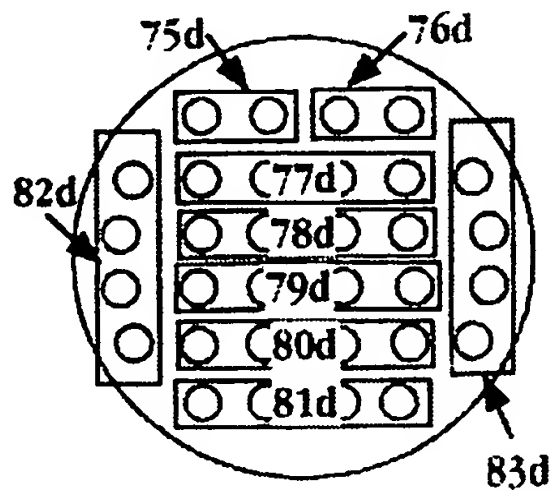


Fig. 7H

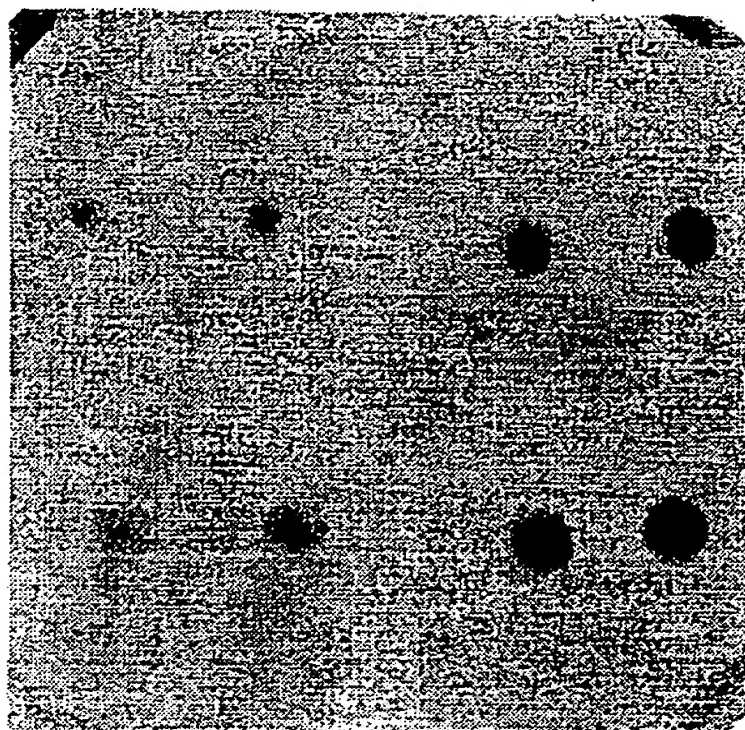


Fig. 8A

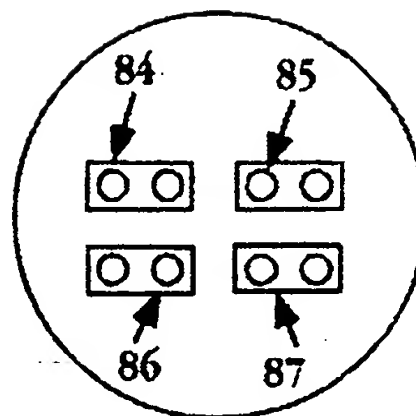


Fig. 8B

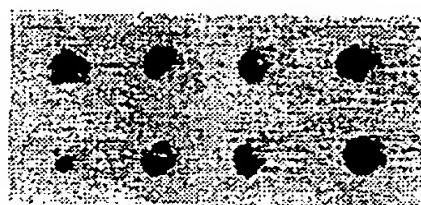


Fig. 9A

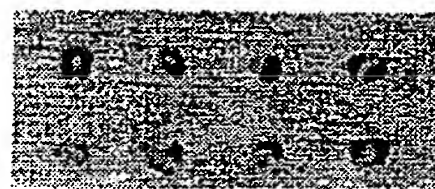


Fig. 9C

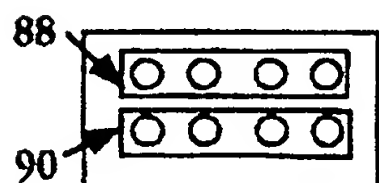


Fig. 9B

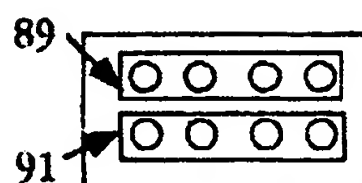


Fig. 9D

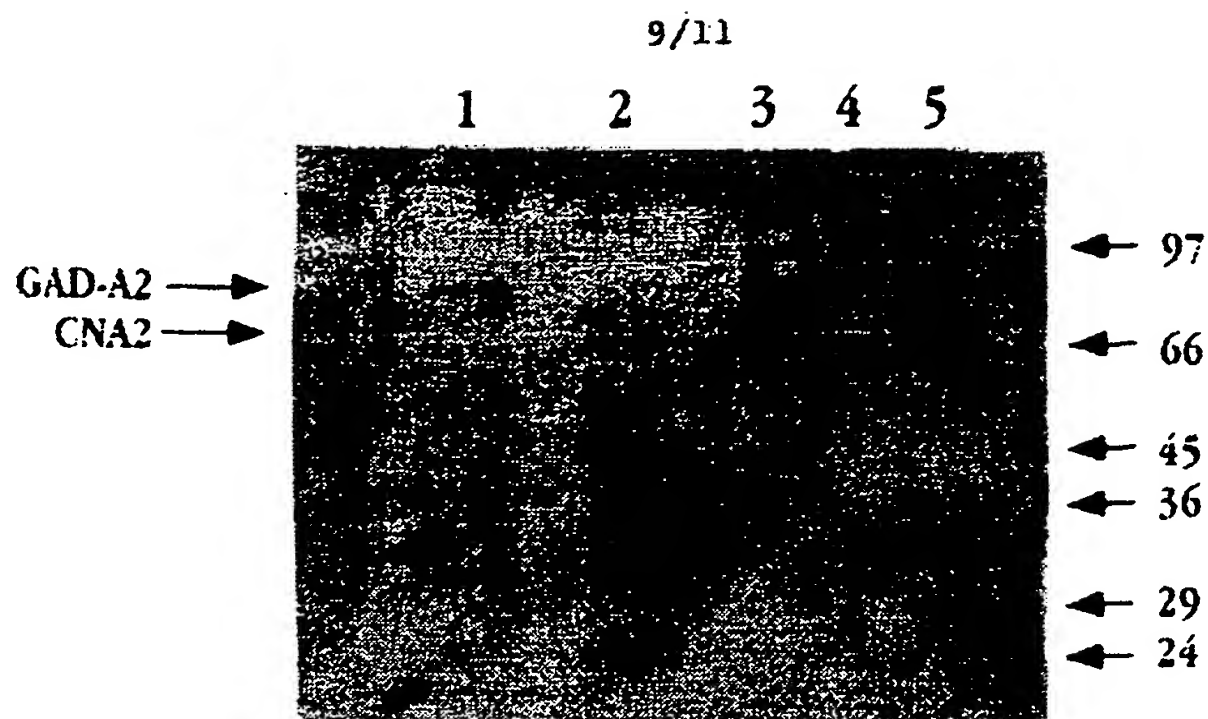
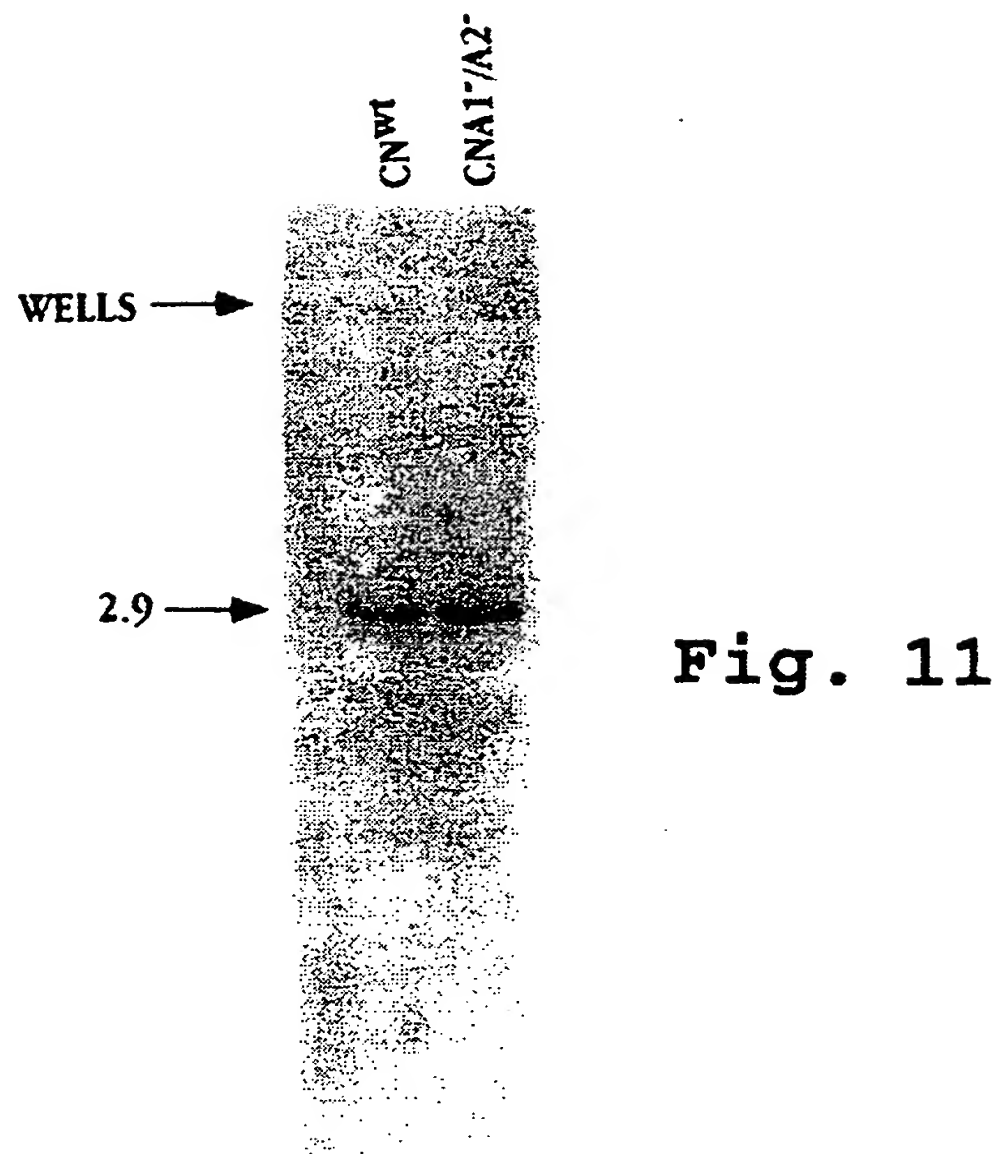


Fig. 10



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10/11

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Fig. 12

11/11

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Fig. 13

INTERNATIONAL SEARCH REPORT

Application No

PCT/US 95/13580

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/395 G01N33/68 C12N15/62 C12Q1/00
C12N1/16 //(C12N1/16,C12R1:865)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Swissprot Database entry YK01_YEAST Accession number P36117; June 01, 1994 Duesterhoeft A. et al.: 'Hypothetical 102.5 kD protein in YPT52-GCN3 intergenic region.'	1-5
X	Emfun Database entry Scykr021w Accession number Z28246; May 10, 1994 Duesterhoeft A. et al.: 'S. cerevisiae chromosome XI reading frame ORF YKR021w.'	6,7
P,X	MOLECULAR BIOLOGY OF THE CELL, 5 (SUPPL.). 1994. 141A., HUANG L ET AL 'A novel protein that interacts with calcineurin in vivo' see abstract 818	1,2,6, 8-15

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☐ Patent family members are listed in annex.

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Date of the actual completion of the international search

21 March 1996

Date of mailing of the international search report

02.04.96

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/13580

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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A	<p>CURR BIOL, 2 (1). 1992. 18-20., CYERT M S 'IMMUNOSUPPRESSANTS HIT THE TARGET' see the whole document -----</p>	